



Mathews,R., Boers,G., den Heijer,M., Kluijtmans,L., van den Heuvel,L. and Rozen,R.  
A candidate genetic risk factor for vascular disease: a common mutation in methylenetetrahydrofolate reductase  
Nat. Genet. 10 (1), 111-113 (1995)

JOURNAL MEDLINE 95375773  
PUBMED 7647779  
REFERENCE 3 (bases 1 to 2196)  
AUTHORS Rozen,R.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAY-1994) Rima Rozen, Pediatrics, Human Genetics and Biology, McGill University - Montreal Children's Hospital, 2300 Tupper St., Montreal, Quebec H3H 1P3, Canada  
4 (bases 1 to 2196)  
Leclerc,D., Sibani,S. and Rozen,R.  
TITLE Direct Submission  
JOURNAL Submitted (29-OCT-1999) Pediatrics, Human Genetics and Biology, McGill University - Montreal Children's Hospital, 2300 Tupper St., Montreal, Quebec H3H 1P3, Canada  
Amino acid sequence update by submitter  
On Nov 2, 1999 this sequence version replaced gi:945022.

REMARK COMMENT Location/Qualifiers  
FEATURES  
source 1.. 2196  
/organism="Synthetic Construct"  
/db\_xref="taxon:32630"  
1.. 2196  
/gene="MTHFR"  
1.. 8  
/gene="MTHFR"  
/note="EcoRI linker"  
13.. 1983  
/gene="MTHFR"  
/note="Method: conceptual translation with partial peptide sequencing"  
/codon\_start=1  
/transl\_table=11  
/product="methylenetetrahydrofolate reductase"  
/protein\_id="AA04440.2"  
/db\_xref="GI:6139053"  
/translation="MVNEARGNSSLNPLEGSSASSGSESSKSDSRCTPGLDPERHER  
LREKMRRLSEGDKNFLEFPPTAEAGVNLISRDRAAGGPYIDVTWPAAGDP  
SDKTSMMIATAVNYGLETILHMTCCORLEPTGHLHAKOLGKKNIALRGDP  
IGDOMEPEGGNVAVDLAKHTRSEGFQDPCVAGYPRGHEBAGSFEADLHKRY  
SAGAPFITOLFEEADTPFRPKACTDMKGTCTIPVPGITGYSRLQVLSTLEK  
PQELKDVEPIKNDNAIKNVGIELVASLQGLASGLVPGHFTLLENMATTEVLK  
RLGMTEDEPRRLPWALSAHPKREDEVPDIPWASPKSYIRTOEMEPGMRGNS  
SSPARGELKDYVLFYLSKSPKEELKMGSELTSEASVEVFLYLSEGPNRNGKV  
TCLPNWDEPLAETSLKEELRVNRGGLTINSOPNIGKPSDPIVGMGSGGVF  
OKAYLEFTRSETAAILOVLKKYELRVNHYLVNKGEMITNAPELQPRAYVWGIFPG  
RRIOTPVDPYSPKFMKDEAFALNIERNGKLYEBSFSRTIIQYIHNYFLVNLVDN  
DPRDNCIMOVVEDTLELNDPTONARETAP"

variation 1298  
/gene="MTHFR"  
/note="E429A: reported by Weisberg et al (1998) Mol. Genet. Metabol. 64, 169-172"  
2196  
/replace="a"  
/gene="MTHFR"  
/note="18 A nucleotides"  
/evidence="experimental"

polyA\_site  
BASE COUNT 482 a 657 c 618 g 439 t  
ORIGIN

Query Match 99.6%; Score 2186.6; DB 12; Length 2196;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 aattccgagagccatggtgacgaagccagaagaaacagcagctcaaccctgtgtgag 60  
|||||  
Db 1 AATTCGGGAGCCATGCTGAACGACGACGAAACAGCAGCCTCAACCCCTGCTTGAG 60  
|||||

QY 61 ggcagtcgcaagcagtcgagagctccaagaagtagtcgagatggttccaccgccggagc 120  
|||||

|||||  
Db 61 GGCAGTCCAGCAGTGGCAGTGAAGAGCTCCAAAGATAGTTGAGATGTTCCACCCGGGC 120  
|||||

QY 121 ctggaacctgagcgcatgtagagactccgggagagaatgtagcgagcttggaaatcgt 180  
|||||

Db 121 CTGGAACCTTAGCGGGCATGAGAGACTCCGGGAGAGATGAGCGCCCATGGATGCTGT 180  
|||||

QY 181 gacaagtgtctcccttggaattctccctccttgaaactgtgtagggagctgtaacttc 240  
|||||

Db 181 GACAAAGTGTTCCTCCGGAATTTCTTCCTCTGAACTGCTGAGGAGACTGTCAATCTC 240  
|||||

QY 241 atctcaaggtttgacggatgtagcagcagctggtgccccctacatagacgttgaactggac 300  
|||||

Db 241 ATCTCAAGGTTTGACCGGATGGCAGAGGTGGCCCTCTCATAGACGTGACTGGCAC 300  
|||||

QY 301 ccagcaggtgacctggtctcaagaagaagaagacctctccatgatatgctgcgcagccgc 360  
|||||

Db 301 CCAGCAGGTGACCTGTGCTCAGACMAAGAACCTCTCCATGATGATCGGCACCGCC 360  
|||||

QY 361 gtgaactactgtgacctgtagaccatctgcacatgacctgtgcgtcagcgctgag 420  
|||||

Db 361 GTGAACACTGTGGCCCTGAGAGACCATCTGCACATGACCTGCTCAGCGCTTGAG 420  
|||||

QY 421 gagatcaaggccatctgcacaaagttaagcaagctgggctgagaaacatcatggtgtg 480  
|||||

Db 421 GAGATCAAGGCGCATCTGCACAAAGCTAAGCAGCTGGGCTGAAGAACATCATGCGCTG 480  
|||||

QY 481 cggggagagaccatagtgaccagtgaggagaagaagaagagcttcaactcagctgt 540  
|||||

Db 481 CGGGAGAACCAATAGGTGACAGTGGGAAGAGAGAGAGGAGGCTTCAACTGACGAGTG 540  
|||||

QY 541 gacctgtgtagacacatcacaagtgagttgtgtactactttgacatctgtgtgagcagt 600  
|||||

Db 541 GACCTGTGTAAGCACATCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600  
|||||

QY 601 taccocaaagccaccccggaagcaggagctttagagctgaactgaagcacttgaagag 660  
|||||

Db 601 TACCCCAAAGCCACCCCGGAAGCAGGAGCTTGTGAGCTGACCTGAAGCATTGAAGAG 660  
|||||

QY 661 aaggtgntgcgggagcgagttcatcatcagcagagtttctttagggtctgacaattc 720  
|||||

Db 661 AAGGTGCTCGGAGCGGATTTTCATATATACCGCAGGCTTTCCTTGTGAGCTGACACTTC 720  
|||||

QY 721 ttccgctttgtagaagcagtcacgcagacatgtagcacttgcgccatcgtcccgagatc 780  
|||||

Db 721 TTCGCTTTGTGAAGCATGACCGACATGAGGATGATGATGATGATGATGATGATGATG 780  
|||||

QY 781 ttcccatccaaggtctacacactcccttcggcagagcttgtgagctgttccaagctggaggt 840  
|||||

Db 781 TTTCCATCCAGGCGTAACACTCCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGGAGGTG 840  
|||||

QY 841 ccaagagagatcaagagcgtgtgtgagccaatcaagaacagatgtgtcaccgcgaac 900  
|||||

Db 841 CCACAGAGATCAAGAGACGTGATTTGAGCCAAATCAAAAGACAGATGTGCTACCCGAC 900  
|||||

QY 901 tatgcatcgaagctgtagcgtgtgagcctgtgccaagagcttgcgcagtggtgtgtgtgca 960  
|||||

Db 901 TATGCGATCGAGCTGGCGCGTGAAGCTGTGCGCAGAGCTTGTGCGCATGTGCTGTGCGCA 960  
|||||

QY 961 ggcctcacttctcaacacctcaacgcgagagatggtctacccaagaagtgcttgaagcgctg 1020  
|||||

Db 961 GGCCTCCTCCTTCAACCCCTCAACCGGAGATGCTACCAACAAGGTGCTGAAGCCGCTG 1020  
|||||

QY 1021 gggatgtgactgagagaccacagcgctccctcactcactcgtcagcttcccaaccacag 1080  
|||||

Db 1021 GGGATGTGACTGAGAGACCCCAAGCGCTCCCTCACTCGGCTTCACTGAGCCACCCCAAG 1080  
|||||

QY 1081 cgcgagaggaagatgtagctcccatcttctggtgctccagacccaagaagttacatctac 1140  
|||||

Db 1081 CGCGAGAGGAAGATGATAGTCCATCTTCTGGGCTCCAGACCAAAAGATTACATCTAC 1140  
|||||

QY 1141 cgtaccacagagatggagagagttccctaaagcgcttggggaattctcttccctgtgc 1200  
|||||

Db	1141	CGAACCCAGAGAGTGGGACGAGATTCCCTAACGGCCGCTGGGGCAATTCTCTTCCCTGCC	1200
QY	1201	tttgggagacttgaagactactactcttctaccitgaagacaagtcctccccaaggaagag	1260
Db	1201	TTTTGGGGAGCTGAAGGACTCTACTCTCTTACTCTGAAGAGCAAGTCTCCCAAGAGAGAG	1260
QY	1261	ctctctaaagctgtggtggggagagagcttganagctgaagcaagtccttgnagtccttgtt	1320
Db	1261	CTCTCTAAAGTGTGGGGGAGAGCTGACCACTGACCAAGTGTCTTTGAAGTCTTGTGTT	1320
QY	1321	ctttaccctctcgggaagaacccaaccggaaatggtacaaagtacttgctctgcccitggaa	1380
Db	1321	CTTTACTCTCTCGGAGAGAACCAACCGGAATGGTCCACAAATGACTTCTGCTGCCCTGGAAC	1380
QY	1381	gatgagcccccttgcgcgttgaagcaagctctctgaagagagagctgctgcgggtgtaaccgc	1440
Db	1381	GATGAGCCCCCTGGCGGCTGAGACCAAGCTCTCTGAAGAGAGAGCTGCTGGGGGTAAACCGC	1440
QY	1441	caaggacatccatccatcaactcaacacagccccaaatacaacggygaagccgctctccgacccc	1500
Db	1441	CAGGGACATCCTCAACCATCACTCACAGCCCCAACATCAACGGGAAGCCGTCTCCGACCCC	1500
QY	1501	atcgttggctgtggggccccagacgggggtatgctttccagaagcctactagatlttctc	1560
Db	1501	ATGCTGGGCTGGGGCCCCACCGGGGGGTATGCTTCTCAGAAAGCCTACTTGAAGATTTTTC	1560
QY	1561	acttcccgcgagacaagcggagaactctcttgaagtgcgtgaagaagtaacgagctccgagtt	1620
Db	1561	ACTTCCCGCGAGACAGCGGAAGCACTTCTCAGATGCTGAAGAAGTACGAGCTCGGGGTT	1620
QY	1621	aattaccaccttctcaatgtgaagggtgaaacaatacaaccaatgtcccctgaactgacgcg	1680
Db	1621	AATTACCACCTTGTCAATGTAAGAGGGTGAAGAAATATCACCAATCCCTGTGAATGCAACCG	1680
QY	1681	aatgcgtcaacttgggggacatcttcccctggcgagagatactaacagccccacgaatgtagt	1740
Db	1681	AATGCTGTACTTGGGGCATCTTCCCTGGCGAGAGATCATCCAGCCCCACCGTAGTGTGAT	1740
QY	1741	cccgttaagcttcatgttcttgggaagacgagagccttgcacctgatatgagtgaagtcggtg	1800
Db	1741	CCCGTAGCTTCATGTTCTGGGAAGGACGAAGCCCTTGGCCCTGTGATTGAGCGGTGGGA	1800
QY	1801	aagctgtatgaagagagatccccgtcccgacacataatccagtaatactcaacgacaactac	1860
Db	1801	AAGCTGTATGAGAGAGAGATGCCCGTCCCGACCATATCATCAGTATCATCCAGCAACTAC	1860
QY	1861	ttccctgttcaacctgtgtgaacaatgacttccacttggacaactgtccctcttgcacgttggtg	1920
Db	1861	TTTCTGTGTAACTGTGTGACATGTACTTCCCTGAGCAACTGCTTGTGGAGTGTGTG	1920
QY	1921	gaagacacatltvgagcttcttcaacaagagcccaacccaagaatgtcgagagaaaagagagctcca	1980
Db	1921	GAAAGACATTTGAGACTTCTCAACAGGCCACCCAGAAATGCGAGAGAAAGGAGGCTCCA	1980
QY	1981	tgaacctgcgtcccttgaagcccttgcgttggagccaactcgttcccgcttccctccactccaca	2040
Db	1981	TGACCTGCTGCTCTGACGCCCTGCGTTGGAGACACACTCTGTCCCGGCTTCTCTCCACACA	2040
QY	2041	gtgcgtctctctcttgggaacttcaactctctcttctgtctctcccaaccccgagctcactc	2100
Db	2041	GTGCTCTCTCTCTTGGGAATCTCACTCTCTCTGTGTCTCTCTCCACCCCGGCTTCACTC	2100
QY	2101	ccccacactgacaatgtgcagctagacttgaagtgtgaagcttccagagcttccctgacctgaag	2160
Db	2101	CCCCACTGTACAATGGCAGCTAGACTGTGAGTGTGAGCTTCCAGGCTCTTCTGTGACACTGAG	2160
QY	2161	tctggccccacatvgggaacctagtactctctgtctcta	2196
Db	2161	TCGGCCCCACATGGGAACCTAGTACTCTGTCTGCTA	2196
RESULT	2		
	447328		

LOCUS	A47328	2219 bp	DNA	linear	PAT 07-MAR-1997
DEFINITION	Sequence 3 from Patent WO9533054.				
ACCESSION	A47328				
VERSION	A47328.1	GI:2301336			
KEYWORDS	.				
SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 2219)				
AUTHORS	Rozen,R. and Goyette,P.				
TITLE	CDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE REDUCTASE				
JOURNAL	Patent: WO 9533054-A 3 07-DEC-1995; UNIV MCGILL (CA)				
COMMENT	Other publication AU 2519895 951221.				
FEATURES	Location/Qualifiers				
source	1..2219				
CDS	/organism="unidentified" /db_xref="taxon:32644" 13..1983 /note="named protein product" /codon_start=1 /protein_id="CAA03053.1" /db_xref="gi:2301337" /db_xref="swiss-prot:P42898" /translation="MVNENRGNSSLNPLCELSASSGSESSKDSRCSPTGLDEPHERH LREKRRRLSEGDKWFSLFEPPTPAEVAVLISRPDMAGGLYIDVTVMHGDGQ SDKESSMMIASTAVNYDGLFTILHMCGRLDEITGHKLAKOLIKNMLRGDP IDQWEEREQGPNYADVLYKIRSEFGYEDPCVAGYKPKHPEASEADLKHLEKV SAGADFIITQLPEADTFRRFVKCTDGIPTVPGIFPIQGHSLROLVKLSLEV POELKDIETPIKNDNALRNYGIELAVALGCELLASGLVPLAHFTLNREMAITEVLR RLGWMTEDPRRLPWLALSAHPKREEDVRPLFMA5SRKSYLYRQEWDEFPNGRWMS SSPAGELKDYLYFLYKSKPKEELKMGSELTSEASVEFVLYLSGPRNHGKVF TCLPNDEPLAETSLKEELLRVNRQILITINSQPNKSPSDPIVGGSGGVYF QKAYLEFTSRETAELIOLVYKKEELRVNRYLNVKGENITNAEPLDPAVTVGIFPG RELIQPLVYDPSPEKQVDEAFALMIERKGLVYEESPSRIIYIDHNTFLVNLVDN DPLIDNCIMOVEVDTELELNRPQNAKTEAP"				
BASE COUNT	501 a 657 c 620 g 441 t				
ORIGIN					
Query Match	99.6%; Score 2186.6; DB 6; Length 2219;				
Best Local Similarity	99.7%; Pred. No. 0; Mismatches 7; Indels 0; Gaps 0;				
Matches 2189; Conservative	0; Mismatches				
OY	1 aattccggaagccaatggtgaacgaagccagaagaaacagacgacctcaacccctgttgag	60			
DB	1 AATTCCGAGCCATGGTGAACGAACCCAGAGAAACAGACGCTCAACCCCTGTGGAG	60			
OY	61 ggcagtgccaggaagtggaagtgagagctcccaagaagtaattgagaagtgttcaacccgggc	120			
DB	61 GGCAGTGCAGGAGTGCGGTGAGAGCTCCCAAGATAGTTCAGATGTTCCACACCCCGGC	120			
OY	121 ctggaacctggaacgagcatagagaactccgggagaagatgagcgagatcttgaaatctggt	180			
DB	121 CTGGACCCCTGACGCGGCATAGAGACTCCGGGAGAAAGATGAGGCGCGCATTTGAAATCTGGT	180			
OY	181 gacaagatggttctccctcggaattcttccctctcgaaactgctgaaggagcgctgtaacttc	240			
DB	181 GACAAGATGTTCTCCCTGGAAATTTCTCCCTCCCAACTGCTGAGGGAGCGTGCMAATCTC	240			
OY	241 atctcaaggtttgaacggagatgcaacagatgagccccctctacatagaagtgtaactggcac	300			
DB	241 ATCTCAAGGTTTGACCGGATGGCAGACAGTGGCCCCCTCTACATAGAGTAACTTGGCAC	300			
OY	301 ccagcaggtgacccctgagctcagaacaaagagacctctccatgatgatctgcacgacggcc	360			
DB	301 CCAGCAGGTGACCCCTGAGCTCAGACAAAGAGAGACTCTCTCATATGATGATGCACGACCGCC	360			
OY	361 gtgaacctactgtgagcttggagacacatctctgaactgactcttcgcgttcagcgcttgag	420			
DB	361 GTGAACCTACTGTGGCTTGGAGACATCTCTGCACATGACCTCTCCGCCGTACCGCTTGAG	420			
OY	421 gagatcagggccacatctgcacaaagctlaagcagcttgagcctcggaagaaacatcatgagcgtg	480			

```
|||||
Db 421 GAGATCACGGGCATCTGCACAAAGCTAAGCAGCTGGCCCTGAAGAAATCATATGCGCTG 480
Qy 481 cgggagagaccataagtgagcaag tgg9aagagagagagagagcttcaactaagcaag t 540
Db 481 CGGGAGAGCCCAATAGTGAGCAGTGGGAGAGAGAGAGGAGCGGTTCACTAGCAATG 540
Qy 541 gactgtgtgaagcaacacccgaagtgtgtgtgtaactacttgacaactgtgtgcaagt 600
Db 541 GACCTGGTGAAGCAATCCGAAAGTGAAGTGTGCTACTTGTGAATCTGTGTGACAGT 600
Qy 601 taccocaaagccaccccgaaagcagagagcttgaagcttgagcttgaagcacttgaagag 660
Db 601 TACCCCAAGGCGCACCCGGAAGCAGGAGCTTTGAGGCTGACCTGAACACTTGAAGAG 660
Qy 661 aaggtgtgtgagagagcagatcattcaatcagcagccttcttgaagctgaagcattc 720
Db 661 AAGGTGTGCGGGAGCGCGATTTTCATCATCAAGCAGCTTTTCTTTGAGGCTGACAGTTC 720
Qy 721 ttccgcttgtgaaagcagatgacacgaatgagcacttgcccaactgtcccgagatc 780
Db 721 TTCCGCTTTGTGAAGGCAATGACACGACATGGGCACTTGCCCATGCTCCCGGAGTC 780
Qy 781 ttccacacagagctacacactccctcgcagactgtgaaagctgtccaaagctgagagtg 840
Db 781 TTTCCCATCCAGGGCTACCACTCCCTTGCGCAGCTTGTGAAGCTGTCCAGCTGAGGAGTG 840
Qy 841 ccacagagatcaagagcagtgatltgagccaatcaaagaacagatgtgtccatccagac 900
Db 841 CCACAGAGATCAAGAGAGAGTATTGAGCCAAATCAAGACAAAGATGTGCCATCCGCAAC 900
Qy 901 tatggcactgagctgagcagctgtgagcagctgtgcaagagcttgcgcaagctgtgtgca 960
Db 901 TATGGCATCTGAGCTGGCGTGTGAGCCTGTGCCAGAGCTTGTGGCCATGTGGCTGTGTGCA 960
Qy 961 ggcctcaactctcaacacctcaacccgagatgtgtctacacagagtgctgaagcgctg 1020
Db 961 GGCCTCACTCTCAACCCCTCAACCGGAGATGGCTACACAGAGTCTGTGAAGCGCTG 1020
Qy 1021 gggatgtgagctgagagcagcagcgtccctacccctgagctgtcagtgtcccaag 1080
Db 1021 GGGATGTGAGCTGAGAGCAGCCAGGCGTCCCTTACCCCTGGCTGTCAAGTCCACCCAG 1080
Qy 1081 cgcagagagagatgtatgctcccatctctgggctcagacaaagatatactac 1140
Db 1081 CGCCAGAGAGAGATGTATGCTCCATCTTCTGGGCTTCACAGCCAAAGATTACTTCTAC 1140
Qy 1141 cgtaccagagatgagcagatctccctaaagcgccgtgggcaattcctctccctg 1200
Db 1141 CGTACCCAGAGATGAGAGATGCTCCCTTAAGCGCCCTGGGCAATTCCTTCCCTGCC 1200
Qy 1201 ttggggagctgaaagactactactcttcttaacctgaagagcaagtcctcccaagagag 1260
Db 1201 TTTGGGAGCTGAAGAGATTACTACTCTTCTTAACCTGAAGAGCAATCTCCCAAGAGAG 1260
Qy 1261 ctgctgaagatgtg9gggagagagctgancagtgaaagcaagtgtcttgaagcttctgt 1320
Db 1261 CTGCTGAAGATGTGGGGGAGAGAGCTGACAGTGAAGCAAGTCTTGAAGTCTTTTGT 1320
Qy 1321 cttactctctcgggagaaacaaaccggaaatgtgtcaaaagtgaactgtccctcggagac 1380
Db 1321 CTTTACTCTCTCGGGAACCAACCGGAATGTGTCAAAAGTGACTTGTGCTCCCTCGGAAC 1380
Qy 1381 gatagagccctcggcgctgaaagcagcctgtctgaagagagagctgtcctcgggtgaagc 1440
Db 1381 GATAGAGCCCTCGGCGCTGAAGACAGCTGCTGAAGAGGAGACTGTCTCGGGTGAAGCCG 1440
Qy 1441 caagggatcctcacatcaatcagcccaacatcaacggaagcgctcctccgaagc 1500
Db 1441 CAGGGATCTCTACACATCACTACAGCCCAACATCAACAGGGAAGCGCTCTCTCGAGCC 1500
Qy 1501 atcgtggctgtgggcccagcgagggtctatgtcttcagaaagcctacttagagttctc 1560
|||||
```

```
Db 1501 ATCGTGGGCTGGGGCCCGGCGGCTATGTCTTCCAGAAAGGCGCTACTAGAGTTTTC 1560
Qy 1561 acttcccgagagacagcggaagcacttctgaagtgctgaagagtlacagctccgggtc 1620
Db 1561 ACTTCCCGGAGACAGCGGAAGCACTTCTGCAGGTGGAAGAAAGTACGACCTCGGGTT 1620
Qy 1621 aattacacacttgaatgtgaaggtgtgaaacatcaccaatgtccctgaactcagcg 1680
Db 1621 AATTACACACTTGTCTAAATGTGAAGGTGAAAACATCACCAATGCCCTGAAACTGAGCCG 1680
Qy 1681 aatgtgtcacttgggagcattccctctggcgagagatcaccagccacagtlagat 1740
Db 1681 AATGTGTCACTTGGGAGATCTTCCCTGGGAGAGATCATCCAGCCACCGTAGTGAT 1740
Qy 1741 cccgtcagctcaatgtctcgaagagagagccttgcctgtagatltgagcggtggga 1800
Db 1741 CCCGTCACTTCAATGTCTGGAAGAGCAGGCGCTTGTGCTGTGATGTGACCGGTGGGGA 1800
Qy 1801 aagctgtatgagagagatcccgctcccgacacatcactcagatataccagacaactac 1860
Db 1801 AAGCTGTATGAGAGAGAGATCCCGCTCCGACACATCATCTCAATCTCACAGCAACTAC 1860
Qy 1861 ttccgtgtcaacactgtgtgacatgacttcccaactgtgcaactgtcctcgtgcaagtg 1920
Db 1861 TTCCGTGTCAACCTGTGTGAGCAATGACTTCCCACTGAGCAACTGCTCTGCGAGGTGTG 1920
Qy 1921 gaagacacatgtgagacttctcaacagcccaacgaatgtcgagagaaacgagagctcca 1980
Db 1921 GAAGACACATTTGAGACTTCTCAACAGGCCCAACCGAATGTGGAAGAAACGAGAGCTTCA 1980
Qy 1981 tgacctgtgtcctgtgagccctcgtgtgagcactcctgtcccgctctcctccaca 2040
Db 1981 TGACCTGTGTCTGTAGCCCTCGCTTGTGAGCCACTCTGTCTCCGCTTCTCTCCACA 2040
Qy 2041 gtctgtctctcttggagaaactcactcctcctgtgtctcctccaccccgctccactc 2100
Db 2041 GTGCTGTCTCTTGTGGAATCTCACTCTCTGCTGTCTGTCTGTCTGTCTGTCTGTCTGT 2100
Qy 2101 cccacactgtcaaatgtgacagctagagtgagaggttccagagcttctccgagcctgag 2160
Db 2101 CCCACCTGTCAAAATGTGAGTGAAGTGAAGCTTGTGTGTGTGTGTGTGTGTGTGTGT 2160
Qy 2161 tcggcccaatgtgaaactgtactctctgtccta 2196
Db 2161 TCGGCCCATGTGGAACCTACTCTCTGTCTTA 2196

RESULT 3
AR097969
LOCUS AR097969 2219 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6074821.
ACCESSION AR097969
VERSION AR097969.1 GI:12807226
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2219)
AUTHORS Rozen, R. and Goyette, P.
TITLE CDNA for human methylenetetrahydrofolate reductase
JOURNAL Patent: US 6074821-A 3 13-JUN-2000;
FEATURES
source 1..2219
BASE COUNT 501 a 657 c 620 g 441 t
ORIGIN
```

Query Match 99.6%; Score 2186.6; DB 6; Length 2219;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy 1 aatlcggagcatgtgtgaacgaagccagaggaacagcagcctcaaacctgtcttgag 60
```



Db 1 AATTCGGACCCATGTGAACGAAGCCAGAAACAGACGCTCAACCCCTGCTGGAG 60  
 Qy 61 ggcagtgccagcagtgccagtgagagctccaagatagtcagagatgttccacccgggc 120  
 Db 61 GGCAGTCCAGCAATGCGAGTGAAGCTCCAAAGATAGTTGAGATTTCCACCCGGGC 120  
 Qy 121 ctgagccctgagcgcagtgagagactccgggagagaatgagcgcgagattggaatcgt 180  
 Db 121 CTGAGCCCTGAGCGCGATGAGAGACTCCGGGAGAGATGAGCGCGCATTTGGAAATCGT 180  
 Qy 181 gacaagtggttcccccgggaatttcccccctgaagactctgagggagcgctgaatctc 240  
 Db 181 GACAGTGGTTCTCCCTGGAAATTTCTCCCTCTGAACTGCTGAGGAGACTGTAATCTC 240  
 Qy 241 atctcaaggtltgacgcgagatgagcagatgagccccctctacatagacgtgacctgac 300  
 Db 241 ATCTCAAGGTTTGACCGGATGGCAGAGTGGCCCCCTCTACATAGACGTGACCTGGCAC 300  
 Qy 301 ccagcagtgagccctgagctcagagaaagagacccctcccatgatatcgccagagaccgc 360  
 Db 301 CCACAGGTGACCTGGCTCAGACAAAGAGACTCTCCATGATGATGGCCAGACCGCC 360  
 Qy 361 gtgacactactgtgctgagagacatctctgacactgacactgtgcgtcagcgctgag 420  
 Db 361 GTGACTACTGTGGCTCGAGACCATCTGACATGACCTGCTGCCGTACAGCGCTGGAG 420  
 Qy 421 gagatcagcgacatctgacacaaagctaaagcagctgagcgctgagaaacatactgagctg 480  
 Db 421 GAGATCAGCGGCCATCTGACAAAGCTAAGCAGCTGGCCCTGAAAGACATATGACCGTG 480  
 Qy 481 cgggagagacccaatagatgagcagtgaggaagagagagagcgcttcaactagcagtg 540  
 Db 481 CGGGAGACCCAAATAGTGAGACACTGGAAAGAGAGGAGGAGGCTTAATTACGAGTG 540  
 Qy 541 gacctggtgaagcacaatccgagatgagttgtggaactcttgacatctgtgtgagcag 600  
 Db 541 GACCTGGTGAAGCACAATCCGAAAGTAGTTGTGTGACTTGTGACATCTGTGTGGCAGT 600  
 Qy 601 taccccaagagccaccccgagcagagagagctttagagctgagcctgaagacatctgaaagag 660  
 Db 601 TACCCCAAGAGCCACCCGAGGAGCAAGAGCTTTGAGGCTGACCTGAACACTTTGAAGAG 660  
 Qy 661 aaggtgtgtgagcagcagatltcatcatcaacgcagcttctctttagagctgacatctc 720  
 Db 661 AAGGTGTGTGAGGAGCGGATTTTCATCATCAAGCGAGCTTTCTTTGAAGGCTGACAACTTC 720  
 Qy 721 ttccgcttgtgaaagagatgacagcagatgagcacttcccatctgttcccgagatc 780  
 Db 721 TTCCGCTTTGTGAAGGCAATGACACGATGGGCACTTGGCCCATGTCGCCGAGATC 780  
 Qy 781 ttcccatcagaggtctaacacttccctcgagcagcttgtgaagctgtgccaagcttgaagtg 840  
 Db 781 TTTCCCATCCAGGGGTACTACACTCCCTTGGCAGCTTGTGAAGCTGTCCAAAGCTGAGGTG 840  
 Qy 841 ccaacagagatcaagagcgtatgttagccaatcaaaagcaacgagtgcctgcacacgc 900  
 Db 841 CCACAGGAGATCAAGGAGGTATGAGCCAAATCAAAAGCAACGATGCTGCATCCGCAAC 900  
 Qy 901 tatgagcatcagagctgagcgctgagacctgtgtccagagagcttctgagcagtgagctgtgca 960  
 Db 901 TATGGCATCGAGCTGGCGCTGAGCTGTGCGAGAGCTTTGCGCAGTGGCTTGGTGCA 960  
 Qy 961 ggcctcacttctataccctcaaacgcgagatgctacccaagagtgctgaagcgctgt 1020  
 Db 961 GGCTCCACTCTTACACCTCAACCGCAGATGCTTACCAAGAGAGTCTGAAGCGCTGT 1020  
 Qy 1021 gggatgtgagatgagagcccaagcggtcccttaccctgagctgagcgtcraagtgcccaacccag 1080  
 Db 1021 GGGATGTGAGTGAAGACCCCAAGCGGTCCCTTACCTGAGGCTCTTAGTGGCCCAAG 1080  
 Qy 1081 cgcagagagaaatgtaactcccttcttgggcttcagagcaaaagttacatctac 1140  
 Db 1081 Cgcagagagaaatgtaactcccttcttgggcttcagagcaaaagttacatctac 1140

Db 1081 CGCCGAGAGGAAGATGTAAGTCCCATCTTCTGGGCGCTCCAGACCAAGAGATTACATCTAC 1140  
 Qy 1141 cgtaccagagagtgaggagagttcccttaacgagcgctggggcaattcccttccctgtgc 1200  
 Db 1141 CGTACCAGAGAGTGGAGCGAGTTCCTTAACGGCGGTGGGGCAATTCCTTCCCTGCG 1200  
 Qy 1201 ttgggagagcttgaagagactactaccctcttacccttgaagagcaagtcctcccaaggagag 1260  
 Db 1201 TTTGGGAGAGCTGAAGACTACTACTCTTCTACCTGAAGAGCAAGTCCCCCAAGAGAGAG 1260  
 Qy 1261 ctgctgaagatgtctggggagagagctgaancagtgaagcaagtgctctngaagtcgtgt 1320  
 Db 1261 CTGCTGAAGATGTGGGGGAGAGAGCTGACCAAGTGAAGCAAGTCTTTGAAGCTTTGTT 1320  
 Qy 1321 ctttacccttcgggagagaaacccggaatggtcaaaaatgactgtgcgccttgaac 1380  
 Db 1321 CTTTACCTTCTGGAGAAACCGGAATGGTACAAAGTACTTGTCCCTGCGCTGGAAC 1380  
 Qy 1381 gatgagcccttgagcgctgagacacagctgtgaaggaagagctgtcgggtgaacgcgc 1440  
 Db 1381 GATGAGCCCTGGGGGCTGAGACCAAGCTGTGAAGGAGAGCTGTGGGTGAACCGC 1440  
 Qy 1441 caaggacatctcaacatcaactcaacagcccaacatacaagcgagagccgtctccgagcc 1500  
 Db 1441 CAGGACATCTCTCAACATCAACTCAACCCCAACATCAACGGGAAGCCCTCTCCGACCC 1500  
 Qy 1501 atcgtgagctgagggcccaagcgaggtatgtcttccagaagagcctaactagagtttcc 1560  
 Db 1501 ATCGTGGGCTGGGGCCCAAGCGGCGCTATGTCTTCCAGAAAGGCTACTTAGAGTTTTC 1560  
 Qy 1561 acttcccgagagacgcgagagcaatctgcaagtgctgaagagatgagagctccgggtt 1620  
 Db 1561 ACTTCCCGGAGAGAGCGGAGAGCACTTCTCAAGTGTGAAGAAAGTACGAGCTCCGGGT 1620  
 Qy 1621 aattaccaccttgcacatgtgaaggtgaaagaaatcaacaaatgcccctgagacgcgc 1680  
 Db 1621 AATTACCACTTGTCAATGTGAAGGTGAAGAAATCAATCAATGCCCTGAACGTGACACCG 1680  
 Qy 1681 aatgtctacatgtggagcatcttccctggcgagagatcaacccaacgacgtatgat 1740  
 Db 1681 AATGCTGACATTTGGGCACTTCTCTGGGCGAAGAGTATCTCCAGCCACCTGATGTGAT 1740  
 Qy 1741 ccggtacagctcatgtctctgaaagagagagccttccctgagatgtgaagcggtggga 1800  
 Db 1741 CCGGTCAAGCTCATGTCTCTGAAAGAGAGAGGCTTTTGCCCTGTGATTTGAACGGTGGGA 1800  
 Qy 1801 aagctgtatgagagagagtcctccgtlcccgacacatcatcaagtaacatccagacatc 1860  
 Db 1801 AAGCTGTATGAGAGAGTCCCGTCCCGGACCATCATTCAGTATCCAGATCCAGCAACTAC 1860  
 Qy 1861 ttccgtgtcaacctgtgtgagacatgacttcccatgtgaacaactgtccctgtgcagtggtg 1920  
 Db 1861 TTCTGTGTCAACCTGTGTGAGCAATGACTTCCCATGTGACAATCTCTCTGTGCAAGTGTG 1920  
 Qy 1921 gaagacacattgagagcttctaacagagcccaacagaaatgagagaaagagagcttca 1980  
 Db 1921 GAAGACACATTGGAGCTTCTTAACAGGCCACCCAGAAATGGAGAAAGAGAGGCTCA 1980  
 Qy 1981 tgaactgtcgtccttgaagcgccctgtgtgagacacatccctgtccgccttccctccaca 2040  
 Db 1981 TGACCTGCGTCTGAGACCCCTGCGTTGAGACCACTCTGTGCGCGCTCTCTCCACA 2040  
 Qy 2041 gtctgtcttcccttgggagacatccatctccctgtgtgtctcccaacccgggctccacac 2100  
 Db 2041 GTGCTGTCTCTTCTGGAAATCACTCTCTCTGTGTCTCTCCACCCGGGCTCTCCACTC 2100  
 Qy 2101 cccaacctgacaatgagcagctagagctgagagcttcccaagcttcttccctgagcgtgag 2160  
 Db 2101 CCCACACTGAAATGAGAGCTAGAGCTGAGAGTGAAGGCTTCAGGCTCTTCCGAGACTGAG 2160  
 Qy 2161 tgggcccacatgggaaactagtaactctctgtctta 2196  
 Db 2161 TGGGCCCCACATGGAACTAGTACTCTGTGCTTA 2196

RESULT 4  
ARI45811 ARI45811 2219 bp DNA linear PAT 08-AUG-2001  
LOCUS Sequence 3 from patent US 6218120.  
DEFINITION ARI45811  
ACCESSION ARI45811  
VERSION ARI45811.1 GI:15109000  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 2219)  
AUTHORS Rozen, R. and Goyette, P.  
TITLE Methods for detecting human methylene tetrahydrofolate reductase  
JOURNAL Patent: US 6218120-A 3 17-APR-2001;  
FEATURES  
source 1..2219  
location/Qualifiers  
BASE COUNT 501 a 657 c 620 g 441 t  
ORIGIN

Query Match 99.6%; Score 2186.6; DB 6; Length 2219;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1 aattccgagacatggtgaacgaagcagaaggaacagcagcctaaccctgcttgag 60  
DB 1 AATTCCGAGACCATGTTGTAACAGACAGAAACAGACCTCAACCCCTGCTTGAG 60  
OY 61 ggcagtgccagcagtgagtgagtgagctcccaagaatgttcgagatgttccacccggag 120  
DB 61 GGCAGTGCACAGAGTGAGAGCTCCCAAGATGATGATGATGATGATGATGATGATG 120  
OY 121 ctgagcccttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180  
DB 121 CTGAGCCCTTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 180  
OY 181 gacaagtgcttcctcctggaattcttcctcctcctcctcctcctcctcctcctcctc 240  
DB 181 GACAAGTGCTTCTCCTCGAATTCTTCCCTCCTCGAAGCTGCTGAGAGAGCTGCTCAT 240  
OY 241 atccaagtgcttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 300  
DB 241 ATCTCAAGGTTGACCGGATGGACAGAGTGCCCTCTCTCATATGACGTGACCTGCG 300  
OY 301 ccaagcagtgacccctggtgtcacaagaagagacccctcctcctcctcctcctcctc 360  
DB 301 CCAGCAGGTGACCTGCTGCTCAGACAGAGACCTCTCTCATGATGATGCGCCAGCAG 360  
OY 361 gtaacactcgttgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 420  
DB 361 GTGAACCTACTGTGGCTTGAGACCATCTCTGACATGACCTGCTGCTGCTGCTGAG 420  
OY 421 gagatcagggccatctgcacaagaagcagaagcagcagcagcagcagcagcagcagc 480  
DB 421 GAGATCAGGGCCATCTGCACAAAGCTTAAGCAGCTGGGCTGGAAGAAATCATGCGGTG 480  
OY 481 cggagagacccaatagtgagcagcagcagcagcagcagcagcagcagcagcagcagc 540  
DB 481 CGGAGAGACCCAATAGTGAGCAGTGGGAGAGAGAGGAGGAGGCTTCACTACGCAATG 540  
OY 541 gactcgtggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 600  
DB 541 GACTCGTGGAGCAATCCGAGTGAAGTGTGTGTGATCTTGTGACATCTGTGTGAGAGT 600  
OY 601 taccccaaaagccaccccggaagcagcagcagcagcagcagcagcagcagcagcagc 660  
DB 601 TACCCCAAAGGCCACCCGGAAGCAGAGGAGCTTTGAGGCTGACCTGAACTTGAAGAG 660  
OY 661 aagtgctnctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 720

DB 661 AAGGTGTGCGGGAGCCGATTTCATCATCAGCAGCTTTCTTTGAGCTTACCATTC 720  
OY 721 ttcgccttgtaagagcatgacccagacatggacacacttgccctcccgagatc 780  
DB 721 TTCGCTTTGTAAAGCATGACCCAGCATGGGATCATCTGCCCCATGCTGCCGGGATC 780  
OY 781 ttcccaatccaggctaccactcccttcggagcagcttgtaagcgtgtccaagctgagtg 840  
DB 781 TTTCCATTCAGAGGCTTACCATCTCTCGGCGAGTGTGAACTGTCCAAAGTGTGAGGTG 840  
OY 841 ccacaggaatcaagagcagtgatgtagcacaatcaagaacacagcagcagcagcagcagc 900  
DB 841 CCACAGAGATCAAGAGCTGATTAAGCCATCAAGACACAGATGCTCCATCCGCCAAC 900  
OY 901 tatggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 960  
DB 901 TATGGCAGCAGCTGGCGGTGAGCTGTGCGAGAGCTTGTGGCAGTGGCTGTGCGCA 960  
OY 961 ggcctccactctacacccctcaaccgagagatggtaccacagagagtgctgagagcagc 1020  
DB 961 GGCTCCACTTCTACACCTCTCAACCGAGATGGCTACAGAGAGTGTGAGAGGCTG 1020  
OY 1021 gggatgtgactgagagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1080  
DB 1021 GGGATGTGACTGAGAGACCCAGGCGTCCCTACCTGGGCTCTCAGTGGCCACCCCAAG 1080  
OY 1081 cgcagagaggaagatgtagtcccaatcttcctgagcagcagcagcagcagcagcagcag 1140  
DB 1081 CGCCAGAGGAAGATGTACGTCCATCTTGTGGGCTCCAGACCAAGGTTACATTCAC 1140  
OY 1141 cgtaccagagtgtagagagatgtccctacacgagcagcagcagcagcagcagcagcagc 1200  
DB 1141 CGTACCAGAGTGAGAGAGATGCTTCCCTAACGCGGCTGTGGGCAATTCCTTCCCTGCC 1200  
OY 1201 ttgggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1260  
DB 1201 TTTGGGAGCTGAAGAGATGATCTTCTTCTTACCTGGAAGAGCAGTCCGCCCAAGAGAG 1260  
OY 1261 ctgctgaagagtgtaggagagcagcagcagcagcagcagcagcagcagcagcagcagc 1320  
DB 1261 CTGCTGAAGATGTGGGGAGAGAGCTGACAGTGAAGAGAGTCTTTGAAATCTTTTGT 1320  
OY 1321 cttaacctcgggagaaaccaaaccggaatggtcaaaagtactgtccctgccttgaaac 1380  
DB 1321 CTTTACCTCTCGGGGAGAACCAACCGGAATGTGTCAAAAGTACTTGTGCTCGCTGGAAC 1380  
OY 1381 gatgagccctcgggagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1440  
DB 1381 GATGAGCCCTTGCGCGCTGAGACAGCCTGCTGAAGAGAGAGCTGTCCGGGTGAACCTGC 1440  
OY 1441 cagggcaltcctacacatcaactcaagcagcagcagcagcagcagcagcagcagcagcag 1500  
DB 1441 CAGGGCATCTCTACCATCACTACAGCCCAACATCAAGGGAAGCCGCTCTCGAGACCCC 1500  
OY 1501 atcgtggcctggggagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1560  
DB 1501 ATCTGGCTTGCGGCGCCAGCGGGGCTATGTCTTCCAGAAAGCCCTACTGTAGATTTTC 1560  
OY 1561 actcccgagagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1620  
DB 1561 ACTTCCCGCAGACAGCGGAAGCACTTGTGCAAGTGTGAAAGAGTACGACTCTCGGGTT 1620  
OY 1621 aattacacactgtcaatgtgaaggtgaagaacatcaccaatgcccctgaaactgcaagcag 1680  
DB 1621 AATTACACACTTGTCAATGTAAGGAGTGAACATCAACATGACCCCTGAACTCAGACCG 1680  
OY 1681 aatcgtcacttgaggagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1740  
DB 1681 AATGCTGCACTTGGGGATTTCTTCCCTGGGAGAGATCAATCCAGCCCTGATGTGGAT 1740  
OY 1741 ccgctcagctcactgtcttgaaagcagagcagcagcagcagcagcagcagcagcagcagcag 1800

Db 1741 CCCCTCAGCTTCATGTTCTGGAAGGACGAGCTTTGCCCTGTGATGACGGTGGGA 1800  
Qy 1801 aagctgatatgagagaggtcccgctcccgacacatccatccagtatccagaactac 1860  
Db 1801 AAGCTGATGAGGAGAGTCCCGCTCCGACACATCATCCAGTACACAGCAAACTAC 1860  
Qy 1861 ttctctgcaacccgtgagaaatgaactcccaacttgacaactctctctgcaagtgtg 1920  
Db 1861 TTCTTGCTCAACCTGTGGAGAAATGACTTCCCACTGGACAACCTGCTTGCGAGTGTG 1920  
Qy 1921 gaagacacattgagactcttcaacagccacccagaatgagagaagaaggagctcca 1980  
Db 1921 GAAGACACATGTGAGCTTCTCAACAGGCCACCCAGATGGAGAGAAACGAGAGCTTCA 1980  
Qy 1981 tgaccctgctcctgagacccctgcttgagacacactctgctccgctctctctccaca 2040  
Db 1981 TGACCTGCGCTGACGAGCCCTGCGTGGAGCCACTCTGTCGCCGCTCTCTCCCA 2040  
Qy 2041 gtgctgctctctctgagaaactccactcctctgctctctcccaaccccgagctcccaac 2100  
Db 2041 GTGCTGCTTCTCTGGAGACTCACTGCTGCTGCTCTCCACCCCGGCTCCACTC 2100  
Qy 2101 ccccaactgacaatgagcagctagactgagtgagcttccagctctctctgagactgag 2160  
Db 2101 CCCCACTGACAAATGAGAGCTAGACTGAGAGGCTTCCAGGCTTCTCTGAGACTGAG 2160  
Qy 2161 tcgccccacatggaacctaactactctctctcta 2196  
Db 2161 TCGCCCCACATGGGAACCTAGTACTCTCTCTCTTA 2196

RESULT 5  
AX356174 2219 bp DNA linear PAT 06-FEB-2002  
LOCUS Sequence 3 from Patent WO0196598.  
DEFINITION AX356174  
ACCESSION AX356174  
VERSION AX356174.1 GI:18620687  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (sites)  
AUTHORS Rozen, R.  
TITLE Cdna for human methyltetrahydrofolate reductase and uses thereof.  
JOURNAL Patent: WO 0196598-A 3 20-DEC-2001;  
MCGill University (CA)

FEATURES  
source Location/Qualifiers  
1..2219  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
13..1983  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAD23022.1"  
/db\_xref="GI:18620687"  
/translation="MYNEARNGNSLNPCLGASGSSGSSKDSRSTPGIDPHERH  
LREKMRRLSEGDGMFSLFEPFRTAEGAVNLISFDDMAAGGLVITDWMHBDGSG  
SOKETSSMIASTAVNYCGLETLHMTCRORLELTGHLAKKQJGDKIMYALRGDP  
IGQWMEEBEGFHYAVDLVKHITSESGDYFDICVAGTPKHPLVGSSEADLHLEKY  
SAGADITITOLFADTFEFVNACTDMGTCPIVGIPIQGYHSLROLVKSLEYK  
POIKNDVIEIRPKNDALIRNYGIELAVSLQELIAGLVGLHFTYLRMATTEVYK  
RLGMTEDEIRRPALMSAHKREDVDVPIFASPKSYITRQWDEPNRMGMS  
SSPAFELKDYLYFLYLSKSPKRELLKMGSEELTSEASVEFVLYLSGPNRGHY  
TCLPMNDEPLAETSLILKEILLBVNROGILITINSOPNKGSPSDPIYSGPSGTYF  
OKAYLEPTSRERAEALLOYLKYELRVNTHLVNKGENTNAPELDPNNAVITGTFPG  
RELIQPTVDPVSFNFWDKDAFALMTERMKLYEESPSTIIQYIHDNFTLVNLVN  
DEPLDNCLMQVVEDTLELNLRPONAREAP."

CDS  
501 a 657 c 620 g 441 t

BASE COUNT 501 a 657 c 620 g 441 t  
ORIGIN

Query Match 99.6%; Score 2186.6; DB 6; Length 2219;

Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 1 aatccgagaccatggtgtaacgaagccagagaaacagcagctcaacccctgttgag 60  
Db 1 AATTCGGAGCCATGTGTAAAGAGCCAGAGAAACACACACCTCAACCCCTGTTGAG 60  
Qy 61 ggcagtgccagcagtgagagtgagagctccaaagatgttgagagtggtccaccgggg 120  
Db 61 GCGAGTGCACAGTAGTGAGAGTGAAGCTCCAAAGTATGTTGAGATGTTCCACCCGGGC 120  
Qy 121 ctggagccctgagcggcagatgagagactccgggagagagatgagagcgagcttgag 180  
Db 121 CTGAGCCCTGAGCGGAGATGAGAGATCCGGGAGAAATGAGAGCGGCGATTGGAATCTGT 180  
Qy 181 gacaagtggtctcccttggaattctccctctcgaactgctgagagagctgtcaatctc 240  
Db 181 GACAAGTGTCTCTCCCTGGAATCTCTCCCTCGAATGCTGTGAGGGAGCTGTCAATCTC 240  
Qy 241 atctcaaggttgaccggatgagcagcagtgagcccccctcaatagacgtgagcttgac 300  
Db 241 ATCTCAAGGTTTGACCGGATGAGACAGGTGAGCCCTCTCATAGACTGACCTGGCAC 300  
Qy 301 ccagcaggtgagccctgagctcagagaaaggaacctctccatgatgatcgccagaccg 360  
Db 301 CCAGAGGTGACCTGGCTTCAGACAAAGAGACCTCTCATGATGATGCGCAGCACCGCC 360  
Qy 361 gtagaactactgtgctctgagagacacactctgacatgacctgctgcgtcagagctgag 420  
Db 361 GTGAAGTACTGTGCTGCGCTGGAGACCATCTGTGACATGACTCTGCGCTGACCGCTTGAG 420  
Qy 421 gagaatcagggccatctgcacaaagctaaagcagctgagcctgagaaacatatgagctg 480  
Db 421 GAGATCACGGGCGCATCTGTACAAAGCTAAGACGTGGGCTGTGAACACATATGGCCTG 480  
Qy 481 cgggagagcccaatagatgagcagtgagaaagagagagagagagcttcaactacagcag 540  
Db 481 CGGGAGAGCCCAATAGGTGAGACAGTGGAAGAGAGAGGAGGAGGCTTCAATACGACAGTG 540  
Qy 541 gacctgtgtagagacacatcccgaaagtgtgtgtgactactcttgacatctgtgtgagct 600  
Db 541 GACCTGTGGAAGCACATCCGAAAGTAGTGTGTGCTTGTGACATCTGTGTGGCAGGT 600  
Qy 601 taccocaaagccaccccgagcagagagcttgagagctgagcctgagaaacattgaagag 660  
Db 601 TACCCCAAGGCCACCCCGAAGCAGAGGAGCTTTGAGGCTGTGACCTGAAGACATTAAAGAG 660  
Qy 661 aaggtgltngcggagccgattcatcatcaacgagcttctcttgagagctgacacatc 720  
Db 661 AAGGTGTCTGGGAGCGGATTTTCATCATACGACGAGCTTTCTTTGAGAGCTGACACATTC 720  
Qy 721 ttccgcttgtagaagcatgacacgacatgagcatcttgcacatctgtcccgagatc 780  
Db 721 TTCCGCTTTGTGAAGGATGACACGACATGGGACATCTTCCCATCTGTCCCGGATC 780  
Qy 781 ttcccatccagggctaccactcccttcgagcagcttgtagagctgtgccaagctgagagt 840  
Db 781 TTTCCTCATCGAGGCTTACACTCCCTTGCGACGCTTGGAAGCTGTCCAACTGGAAGTG 840  
Qy 841 ccacagagatcaagagcgtgattgagccaatcaaaagacaaagatgctgcatccgcaac 900  
Db 841 CCACAGAGATCAAGAGACGTGATTGAGCCAAATCAAAAGACAAAGATGCTGCATCCGCAAC 900  
Qy 901 tatgcatcgagctgagccggtgagagctgtgccaagagcttctgccaagtgtgtgtgcca 960  
Db 901 TATGCGATCGAGCTGCGCGTGAGGCTGTGCGAGAGCTTCTGGGCAATGGCTGTGTGTCCA 960  
Qy 961 ggcctcactctacacccctcaaccgagagatggtcaccacagaggtgtgtaagcgctg 1020  
Db 961 GGCTTCACCTTCTACACCTTCAACCGGAGATGGCTACACAGAGGTGCTGAAGCGCTGTG 1020  
Qy 1021 ggaagtgtgagctgagagccccaagcgctccctacactgagctctcaagtgcccaaccgaag 1080  
Db 1021 GGAAGTGTGAGCTGAGAGCCCAAGCGCTCCCTACACTGAGCTCTCAAGTGCACACCCGAAG 1080

```

Db 1021 GGGATGTGAGTGAAGACCCAGGCGTCCCTACCTGGGCTCTCAGTCCACCCCAAG 1080
Oy 1081 cgcgagaggaagatgtaagctccatctcttgagcctccagacaaagattacatctac 1140
    |||||||
Db 1081 CGCGGAGAGGAATGATGACTCCCATCTTCTGTGGCCCTCCAGACCAAGAGATTACATCTAC 1140
Oy 1141 cgtaccagagagtgagagcagatctccctaagcgccgtgggcaattctctccctgac 1200
    |||||||
Db 1141 GGTACCCAGAGAGTGGGACGAGTTCCCTTACGGCCGCTGGGGCAATTCTTCCCTCCGCC 1200
Oy 1201 ttggagagagtgagagagctactactctcttactactgaagagcaagtcctccaaagagag 1260
    |||||||
Db 1201 TTGGGAGAGCTGAAGAGCTACTACTCTTCTACTGAAAGCAAGTCCCCCAAGAGAGAG 1260
Oy 1261 ctgctgaagatgtgagggagagagctgancagtgaaagagtgctcttngaagcttgct 1320
    |||||||
Db 1261 CTGCTGAAGATGTGGGGGAGAGCTACACAGTGAACCAAGTCTTGTGAAGTCTTGT 1320
Oy 1321 cttaactctcgagagagacaaacagagatggtacaaagtactctgagccttggaac 1380
    |||||||
Db 1321 CTTTACTCTCGGAGAACCAACCGAATGCTACAAAGTACTGCTGCTGCTCCCTGGAAC 1380
Oy 1381 gatgagcccttgagcgtgagagcagccctgctgaagagagagctgctgaggtgtaaccgc 1440
    |||||||
Db 1381 GATGAGCCCTGGCGGCTGAGACCAAGCTGCTGAAGAGAGAGTGTGCGGGTGAACCGC 1440
Oy 1441 cagagacatccctccacatcaactcacagccaaacaaacagggagagcgtctccgagccc 1500
    |||||||
Db 1441 CAGGCAATCCCTCACATCAATCAACAGCCCAATCAACGGGAGAGCCGCTCCGACCCC 1500
Oy 1501 atcgtgagcgtgagggcccaagcgggagtgatgctctccagaagagctactagagatttctc 1560
    |||||||
Db 1501 ATCGTGGGCTGGGCCCCCAGCGGGGGCTATGCTTCCAGAAAGGCTACTTAGAGATTTC 1560
Oy 1561 actcccgagagagagcggagagcactctctgcaagtgtctgaagagagctcagagctcggtt 1620
    |||||||
Db 1561 ACTTCGCGGAGACAGCGGAAGCACTTCTGCAAGTGTCTGAAGAGAGTACAGACTCCGGGT 1620
Oy 1621 aattaccacctctgcaatgtgaaggtgaagaacaaacaaatgcccctgaactgaagcgc 1680
    |||||||
Db 1621 AATTACCACTTGTCAATGTGAAGGCTGAAMAATCAACCAATGCCCTCGAAGCTGAGCGG 1680
Oy 1681 aatgctgcaacttgagagcattctccctggagcgagagatcacccagccacgtatgtagt 1740
    |||||||
Db 1681 AATGCTGTCACTTGGGAGATCTTCCCTGGGAGAGATCAACAGCCACGCTAGTGGAT 1740
Oy 1741 cccgtcaactcattgctctggaagagagagccttgcctgtagattgagcgtgtaggga 1800
    |||||||
Db 1741 CCGGTCACTTCATGTTCTTGGAAAGAGAGAGCTTTGCCCTGTGGATTGAGCGGTGGGA 1800
Oy 1801 aagctgtatgagagagagatccccctgccagacatcacatccagttacatccagacatcac 1860
    |||||||
Db 1801 AAGCTGTGTGAGAGAGATCTCCCGTCCGACATCAATCAATCAACGACACAACTAC 1860
Oy 1861 ttctctgtaacacctggtggaacatgaacttcccaatggaacactgctcttgcaagtggtg 1920
    |||||||
Db 1861 TTCTCTGTCAACCTGTGTGACAAATGACTTCCACAGTGAACATGCTGTGGCAGGTGGTG 1920
Oy 1921 gaagacacatgtgagctcttccaaagcgccacccagaaatgcagagagaaacggaagctcca 1980
    |||||||
Db 1921 GAAGACACATGTGAGACTTCTCAACAGGCCACCCAGAAATGGAGAGAAACGAGAGCTCCA 1980
Oy 1981 tgaccctgtctctgaagcctctggttgtagaacactctctgcccgccttccctccaca 2040
    |||||||
Db 1981 TGACCTGTGCTCTGACCCCTGCGCTGTGAGACACTCTCTGTCGCCCTTCTCTCTCCACA 2040
Oy 2041 gtctgctctctcttggaactccactctctctgctctctcccccagcgtccactc 2100
    |||||||
Db 2041 GGTGCTGTCTCTGTGGAACTCCACTTCTCTGCTCTCTCCACCCCGGCTCCACTGC 2100
Oy 2101 ccccaactgacaatgagcagctagagctgagagcttccagagctctctctgagactgag 2160
    |||||||
Db 2101 CCCCACCTGACAAATGAGAGTGAAGTGAAGGCTTCAGAGCTTCTCTGAGACTGAG 2160

```

```

Oy 2161 tggccccacatgagagacctaagtagtactctgtctcta 2196
    |||||||
Db 2161 TGCGCCCCACATGAGAACTAGTACTCTGTGCTTA 2196

RESULT 6
LOCUS A47326 2220 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 1 from Patent WO9533054.
ACCESSION A47326
VERSION A47326.1 GI:2301334
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2220)
AUTHORS Rozen, R. and Goyette, P.
TITLE cDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE REDUCTASE
JOURNAL Patent: WO 9533054-A 1 07-DEC-1995;
UNIV MCGILL (CA)
COMMENT Other publication AU 2519895 951221.
FEATURES
Source location/Qualifiers
1..2220
/organism="unidentified"
/db_xref="taxon:32644"
1..1980
/note="unnamed protein product; protein sequence is in
conflict with the conceptual translation"
/codon_start=1
/protein_id="CAN03052.1"
/db_xref="GI:2301335"
/translation="NSGAVNNEARGNSLNPCLIESAGSSSESXSDSRKSTPGIDPE
RHERLEKMRRLRLESGDKWFSLEFPPTAEAGVNLISFRDHAAGGPLYIDVTHPA
GDPGSDKETSMMIASTAVNYGLETILHMTCCORLEETIQLHKAQGLKNTMAL
RDPIDGDMEEEGGFNYADVLKHIRSEFGFDICVAGYKRGHDEAGSFADLKHL
KEKVSAGADPIITOLFPEADTFEPYKACIDMGITCPIYVGFIFPIOGYIFSLQVLKLS
KLKVPQIDVPIPIKDNDATIRNGLIELAVLSICORLISGLVPLGHEFTLREMAAT
ELVRIGMTEDEDRRLPMALSHNRPREDEVRPIPMASRPKSYIKROEMDFPMGR
WGNSSSPARELIDVLYLYLKSPPAEELKMGELTSEASVFEFVLYLSGERPRN
GHRVCTLPNMDPLAETSLKSELIRVNRGILLTINSQPNINGKPSDPIVGMPSG
GYVFOKAYLEFETSRTEALQLQVLYELRVNHLVNYGENTINAPLQPNAYTVN
IFPGRLEIOTVDPVSPFMKDEAFALMTERNGKLYEESESPSRITIOYIHNYELVN
LVNDPRLDNCIMQVEDTLELNRPTONARETAP"

BASE COUNT 501 a 658 c 620 g 441 t
ORIGIN

Query Match 99.6%; Score 2186.6; DB 6; Length 2220;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

```

Db 301 CCGAGGAGTACCTGGCTAGACAAAGAGACCTCTCCAGAGATCGCCAGACCGCC 360
Qy 361 gtaactactgtgctcggagacatctgcatactgctcgtcgcctgagcgtgag 420
Db 361 GTGAACACTGTGGCCCGAGAGACCATCTGACATGACCTGCTCCGTCAGCGCTGGAG 420
Qy 421 gagatcagggccatctgcacaaagctaagcagctggcctgaaagaaatcatgctg 480
Db 421 GAGATCACGGGGCATCTGCACAAAGCTAACGAGCTGGGCTGAAGAACATCATGCGCTG 480
Qy 481 cggggagaccatagtgccagtggaagaggaggaugaggcttcaactacgcaagt 540
Db 481 CGGGAGACCCAAATAGGTGACCAAGTGGAAAGAGAGAGGAGGCTTCACTTACGCAAGT 540
Qy 541 gacctgtgagacacatcccaagtgaattgtgtaactcttgacatctgtgctgagct 600
Db 541 GACCTGTGAGACACATCCGAGAGATTTGGTACACTTTTGACATCTGTGTGGCAGGT 600
Qy 601 taacccaagagcaccacccaagcaggagcttgaggctgacctgaaacacttgaaag 660
Db 601 TACCCCAAGGCCACCCGAGAGCGAGGAGCTTGAGGCTGACCTGAAGCACTTGAAGAG 660
Qy 661 aaggtgtgacggagcggatccatcatcacagcagcttcttgagcgtgaaacatc 720
Db 661 AAGGTGTCTCGGAGCCGATTTCAATCATACGAGCTTTCTTGAAGCTGACACATTC 720
Qy 721 ttccgcttctgaaagcagcaccgacatgagcagcttgacccatcgtcccgagct 780
Db 721 TTCGGTTTGTGAAGCATGACGACATGAGGATGAGGATGATGATGATGATGATGATG 780
Qy 781 ttcccatccagagcttaccatcccttcgcaactgctgcaactgctgcaactgca 840
Db 781 TTTCCATCCAGGGCTACCACTCCCTGGACCTTGTGAAGCTGTGCAAGCTGAGAGTG 840
Qy 841 ccacagagatcacaagagcgtgattgagccacatcaaaagacagatgctgacatcc 900
Db 841 CCACAGAGATCAAGAGCGATGATTGAGCCATCAAAAGACACATGCTGCTATCCGAC 900
Qy 901 tatgagatcgagctgagcgtgagcgtgctgcaagagcttctgcaagctgctgag 960
Db 901 TATGAGATCGAGCTGCGCGGAGCTGTGTCAGAGACTTGTGCGCAGTGTGCTGCTG 960
Qy 961 ggcctcaacttctacacccctcaacggagatgctacacacagagatgctgcaag 1020
Db 961 GGCCTCACTTCTACACCTTCAACCGGAGATGCTACCAAGAGTGTGGAAGCGCTG 1020
Qy 1021 gggatgtgactgaggaacccaagcgctccctacacctgctgcaagctgctgca 1080
Db 1021 GGGATGTGACTGAGGAGCCCAAGGCGTCCCTACCTGCGCTCTCAAGTGCCTCC 1080
Qy 1081 cgcggagaggaagatgtagtcccatctctgggctccagacaaagattacatctac 1140
Db 1081 CCGCGAGAGGAAGATGTAGCTCCATCTTCTGGGCTCCAGACCAAGAGTGTACATCT 1140
Qy 1141 cgtacccaagatgaggaagatccctcaacggcggctggggaattcccttcctg 1200
Db 1141 CGTACCCAGAGATGGAGACAGTTCCTTAACGGCCGCTGGGCAATTCCTTCCCTG 1200
Qy 1201 ttggggagctgaaagactactactcttctacactgaaagaaagctccccaag 1260
Db 1201 TTTGGGAGCTGAAGACTACTACTCTTCTACTGTAAGAGCAAGTCCCAAGAGGAG 1260
Qy 1261 cgtcgaagatgtggggaggaagctgancatgaaagcaagtgctctgaaagtctt 1320
Db 1261 CTGCTGAAGATGTGGGGAGGAGCTGACCACTGAAGCAAGTGTCTTAAAGCTTTGT 1320
Qy 1321 cttaactctcggagaaaccaacggaaatgttcaaaagtactgctgctccctgga 1380
Db 1321 CTTTACCTCTCGGAGAACCAACCGGAATGTCTCAAAAGTACTTGTGCTCCCTGGA 1380
Qy 1381 gatgagccctgagcgtgagacacagcctgctgaaaggaagctgctgagggtga 1440

```

```

Db 1381 GATGAGCCCTCGGGGCTGAGACCAAGCTGCTGAAGAGAGACTGTCGGGGTGAACCG 1440
Qy 1441 caggacatctccacatcaactcaagcccaactcaacggaaagcgtctctccgaccc 1500
Db 1441 CAGGACATCTCCACATCAACTCAAGCCCAACTCAAGGGAAGCGCTCTCCGACCC 1500
Qy 1501 atcgtgggctggggcccaagcggggtatgtcttcagaagagcctaataagttctc 1560
Db 1501 ATCGTGGGCTGGGGCCCAAGCGGGGCTATGTCTTCCAGAAAGCTTACTTAAGATTTC 1560
Qy 1561 acttcggcagagacagcgaagcactctcgaagtgtgaaagaaagtaagactccg 1620
Db 1561 ACTTCGGCGAGACAGCGGAAGCACTTCTGCAATGCTGAAGAAAGTACGAGACTCC 1620
Qy 1621 aattacacacttgcattggaagygtaaacatcaacaaatgcccctgaaactgca 1680
Db 1621 AATTACCACTTGCATATGTGAAGGTGAAGAAACATCAACCAATGCTCCCTGAAC 1680
Qy 1681 aatgtctcacttggggacatctccctggcgagagatcaaccagccacgtatgat 1740
Db 1681 AATGCTGCACTTGGGCACTTCTCCCTGGCGAGAGATCATCCAGCCACCTGATGAT 1740
Qy 1741 ccgctcagctcatgtctcgaagagcagagccttggcctgtagatgagcgtgg 1800
Db 1741 CCGCTCAGCTTCAATGTTCTGGAAGAGAGAGGCTTTCCTTGAGATTGAGCGGTG 1800
Qy 1801 aagctgtaagagagagagctcccgctccgacacatcaaccagatccagacac 1860
Db 1801 AAGCTGTATGAGAGAGAGTCCCGTCCGACATCATCAATGATCATCAAGCAACTAC 1860
Qy 1861 ttccgtgcaacctgctgcaaatgacttcccaactggacaaactgctcgtcagtg 1920
Db 1861 TTCCTGTCAACCTGGTGGCAATGACTTCCCATGAGCAAACTGCTGCGAGGTG 1920
Qy 1921 gaagacacatgtgagctcttccaaagggcccaacccaatgagagaaagagagct 1980
Db 1921 GAAGACACATGTGAAGCTTCTCAACAGGCCCAACAGATCGAGAAAGGAGGCTCCA 1980
Qy 1981 tgacccctgctcctgagacccctgctgttgagacacccctgtcccgcttccct 2040
Db 1981 TGACCCCTGCTCCTGAGACCCCTGCTGTGAGCCACTCTCTCCGCTTCTCTCACA 2040
Qy 2041 gtgctgcttctctgggaactcaactctctcgtgtctctcccaacccgctcact 2100
Db 2041 GTGCTGCTTCTTGGGAATCACTCTCTCTGTGCTCTCCACCCGCGCTCCACTC 2100
Qy 2101 ccccaactgcaatgtgcaagtagactgaggtgaggttccaggtcttctctgaa 2160
Db 2101 CCCCACTGCAATGTGCACTGAGTGAAGGCTTCCAGGCTTCTCTGAGACCTGAG 2160
Qy 2161 tcggcccaatgagaaactagactctctgctca 2196
Db 2161 TCGGCCCAATGTGAACCTAGTACTCTGTGCTCA 2196

RESULT 7
LOCUS AR097968 2220 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6074821.
ACCESSION AR097968
VERSION AR097968.1 GI:12807225
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2220)
AUTHORS Rozen,R. and Goyette,P.
TITLE CDNA for human methyltetrahydrofolate reductase
JOURNAL Patent: US 6074821-A 1 13-JUN-2000;
FEATURES
source 1..2220
BASE COUNT 501 a 658 c 620 g 441 t

```





```

QY 2101 cccaccatgacaatgacagctagactggaagtgaagcttccagctcttccctggagcctgag 2160
      |||
Db 2101 cccactactgacaaatggagagctagactggaagtgaagcttccagctcttccctggagcctgag 2160
QY 2161 tcggcccacatggaagaaactagtaactctctgctcta 2196
      |||
Db 2161 tcggcccacatggaagaaactagtaactctctgctcta 2196

RESULT 8
ARI45810 ARI45810 2220 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 1 from patent US 6218120.
ACCESSION ARI45810
VERSION ARI45810.1 GI:15108999
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2220)
AUTHORS Rozen, R. and Goyette, P.
TITLE Methods for detecting human methylene tetrahydrofolate reductase
JOURNAL Patent: US 6218120-A 1 17-APR-2001;
FEATURES
SOURCE location/Qualifiers
      1..2220
      /organism="unknown"
BASE COUNT 501 a 658 c 620 g 441 t
ORIGIN

Query Match 99.6%; Score 2186.6; DB 6; Length 2220;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2186; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 aattccggaagcattggtgaaacgaagccagaggaacacagcagcctcaacccctgcttgag 60
Db 1 AATTCCGGAGCCATGGTGAACGAAGCCAGGAACAGACACCTCAACCCCTGCTTGGAG 60
QY 61 ggcagctgcagcagatgagcagtgagagctccaaagatgttgaagatgttccaccccgagc 120
Db 61 GGCAGTGCACAGATGAGAGTGAAGCTCCAAAGATGATTGAGATGTTCCACCCCGAGC 120
QY 121 ctggaacctgagcgagcatgagaagactccgagagagaagatgagcgcgatggaatctggt 180
Db 121 CTGGAACCTGAGCGGCAATGAGAGACTCCGGAGAAAGATGAGCGCGCATTTGGAAATCTGT 180
QY 181 gacaagtggtctccctggaattcttccctcctcgaactgcttgagagagctgtcaatctc 240
Db 181 GACAAGTGGTTCCTCCCTGGAATTCTTCCTCTCGAATCTGTGAGGAGCTGTCAATCTC 240
QY 241 atccaaggtttgacccgagatgacagcaggtggcccccctcaatagacgtgacctgagac 300
Db 241 ATCTCAAGGTTTGACCCGATGACAGAGTGGCCCCCTCTACATAGACGTGACCTGGGAC 300
QY 301 ccagcaggtgacctggtctcagacaagagagacctctccatgatgatgcagcaacgcgc 360
Db 301 CCAGCAGGTGACCTGCTCTCAGACAAAGAGACCTCTCCATGATGATGCCAGCACCCGC 360
QY 361 gtgaactactgtgcttggagacacactctgacatgacctgtgctgctcagcgctgag 420
Db 361 GTGAACCTACTGTGGCTTGAGACACTCTGACATGACCTGCTGCTGCTGAGGAGCTTGAG 420
QY 421 gagatcagggccatctgcacaaagttaagcagctggcgctgaggaacatcatggcgctg 480
Db 421 GAGATCAGGGCCATCTGCACAAAGCTTAAGCAGCTGGCGCTGGAAGACATCATTTGGCGCTG 480
QY 481 cggggagagcccaatagtgagcagtggtgaaagagagagagaggttcaactaagcagtg 540
Db 481 CGGGGAGAGCCCAATAGTGAGCAGTGGGAAAGAGGAGGAGGAGGCTTAACTACCGCAATG 540
QY 541 gacctggtgaagacacatccgaagtgtgtgactacttgatcatctgtgtgagcagtg 600

```

```

Db 541 GACCTGGTGAAGACATCCCAAGTACTTGGTACTTATGACATCTGTGGGAGGT 600
QY 601 taacccaaagccaccgccgaagcagagagctttgaggctgacctgaagcacttgaagag 660
Db 601 TACCCCAAAGCCACC GCCGAAGCAGGGAGCTTTGAGGCTGACCTGAAGCACTTGAAGAG 660
QY 661 aaggtgntgcggagagcgagttcatcatcagcaggtttctttgaggtgacacatc 720
Db 661 AAGGTGNTGCGGAGAGCGAGTTTCATCATACGAGGCTTTCTTTGAGGCTGACATTC 720
QY 721 ttccgcttggaaagcatccaccgacatgagcacttgccccatcgtccccggagac 780
Db 721 TTCCGCTTTTGAAGGATGACCATCGACATGAGGATCATCTTGCCCATCGTCCCGGAGATC 780
QY 781 ttcccatcgaagggctacacactcccttcggcagctgtgaaagctgttccaagctggaggtg 840
Db 781 TTTCCTCATCCAGGGCTACCACTCCCTTCGGCAGCTTGTGAAGCTGTCCAAGCTGAGGTG 840
QY 841 ccacagagaatcgaagacgctgattgagccaatacaagaacagatgctgcacatccgaac 900
Db 841 CCACAGAGATCAAGAGACGATGATTGAGCCATCAAAAGACATGCTGCTGATCCGCAAC 900
QY 901 tatgcatcagagctgagcgtgagcctgtgcagaagacttctgacagctggtgtgcca 960
Db 901 TATGCAATCAGAGCTGAGCGCTGAGAGCTGTGCCAGAGCTTCTGCGCACTGTGCTCCA 960
QY 961 ggcctcaactctacacccctcaacgcgagatgagctacacagaaggtgtgaaagcgctg 1020
Db 961 GGCCTCAACTCTACACCCCTCAACCGGAGATGAGCTACACAGAGAGCTGTGAAGCGCTG 1020
QY 1021 gggatgtgagactgagacccccaagcgctccctacaccttgagctcagtgccacccaag 1080
Db 1021 GGGATGTGAGACTGAGACCCCAAGCGCTCCCTACCTTGAGCTGTCAATGCTCCACCCCAAG 1080
QY 1081 cgcggaagagagatgtgaagcttccatcttctgggctcccaagaagagttacatctac 1140
Db 1081 CGCGGAGAGAGATGTGAAGCTTCCATCTTCTGGGCTCCCAACCAAGAGTTACATCTAC 1140
QY 1141 cgtaacccagagtgtagcagagttccctcaacgcgcgtgtgggcaattctcttccctgac 1200
Db 1141 CGTACCCAGAGTGTGAGAGTTCCTCAACCGGAGATGAGCTGTGGGCAATTCTCTCCCTGAC 1200
QY 1201 ttggggagctgaaagactactacactcttcaactgaagagcaagctccccaagagagag 1260
Db 1201 TTTGGGAGCTGGAAGGACTACTACTCTTCTTCACTGAAGACCAAGTCCCTCCCAAGAGAG 1260
QY 1261 ctgctgaagatgttgaggagagagctgancagtgaagcaagtgtcttngaaagcttctgt 1320
Db 1261 CTGCTGAAGATGTGAGGAGAGAGCTGACAGTGAAGCAAGTGTCTTGAAGTCTTTGTT 1320
QY 1321 cttaacctctcggaagaaaccaaaccggaatgtcaaaagtgaactgctgacctgagac 1380
Db 1321 CTTTACCTCTCGGAGAAACCAACCGGAATGTCAAAAGTGAAGTCTGCTCTCTGGAAC 1380
QY 1381 gataagccccctggcggtgagaaacagcctgctgaaagagagagctgctgaggtgaaagcgc 1440
Db 1381 GATAGCCCCCTGGCGGCTGAGAACCAAGCTGTGAAGGAGAGAGCTGTCTGGGTGAACGC 1440
QY 1441 caagagcatcctcacatcaactcaacagccacaactcaacagggagagcgcttcccgacccc 1500
Db 1441 CAGGAGCATCTCACCATCAACTCAACAGCCCAATCAACGGGAGAGCGTCTCCGACCCC 1500
QY 1501 atcgtgggctggggcccccagcggggctagtcttccagaagagcctacttagaatttctc 1560
Db 1501 ATCGTGGGCTGGGGCCCGCCAGCGGGGCTATCTCTTCCGAAGGCTTACTTAGAATTTTTC 1560
QY 1561 aattcccgagagacagcggaagcacttctgcaagtgtgaaagagtiacagactccgggt 1620
Db 1561 ACTTCCCGAGAGACAGCGGAAGCACTTCTGCAAGTGTGCAAGAGTACAGACTCTCGGGTT 1620
QY 1621 aattaccactgttcaatgtgaaggtgaaaaacatcaccaatgccccgaactgagcagcg 1680

```





```

Db 901 TATGCATCGAGCTGGCCGTGAGCCCTGTGCCAGAGACTTCTGGCCAGTGGCTTGCCCA 960
Qy 961 ggcctcaactctacacccctcaacgcgcagatgtgtctaccacagagggtgtcgaacgcctg 1020
Db 961 ggcctcaactctacacccctcaacgcgcagatgtgtctaccacagagggtgtcgaacgcctg 1020
Qy 1021 gggatgtgagctgaagagcccaaggcgtccctacccctgctcagtcagtcgaaccccaag 1080
Db 1021 gggatgtgagctgaagagcccaaggcgtccctacccctgctcagtcagtcgaaccccaag 1080
Qy 1081 cgcgcagagagaaatgtagctccatctctctgagcctccagaccacaaagatccatctac 1140
Db 1081 cgcgcagagagaaatgtagctccatctctctgagcctccagaccacaaagatccatctac 1140
Qy 1141 cgtaccacagagatgagagagatcccttaacgycgcgtgaggcaatctctctccctgccc 1200
Db 1141 cgtaccacagagatgagagagatcccttaacgycgcgtgaggcaatctctctccctgccc 1200
Qy 1201 ttggggagagctgaagagatctctacccctctctacctaagaagagagagagagagag 1260
Db 1201 ttggggagagctgaagagatctctacccctctctacctaagaagagagagagagagag 1260
Qy 1261 ctgctgaagatgtcgggggagagagctgancagtgaaagcaagtgtctnagaagctctgtc 1320
Db 1261 ctgctgaagatgtcgggggagagagctgancagtgaaagcaagtgtctnagaagctctgtc 1320
Qy 1321 cttaactctcgcggagagaccaaaccgggaatgtcacaagatgactgtgctcctcggagac 1380
Db 1321 cttaactctcgcggagagaccaaaccgggaatgtcacaagatgactgtgctcctcggagac 1380
Qy 1381 gatgagccctctgagcgtgagacagcgtctgaagagagagctgctgagcgtgagacgcg 1440
Db 1381 gatgagccctctgagcgtgagacagcgtctgaagagagagctgctgagcgtgagacgcg 1440
Qy 1441 caaggcatcctcacatcaactcaacagccaacatcaagcggaagccgctcccgacccc 1500
Db 1441 caaggcatcctcacatcaactcaacagccaacatcaagcggaagccgctcccgacccc 1500
Qy 1501 atcgtgagcgtgagagcccaacgcggagctgctcctcagaagagagagagagagagag 1560
Db 1501 atcgtgagcgtgagagcccaacgcggagctgctcctcagaagagagagagagagagag 1560
Qy 1561 acttcgcgcagagacagcggaagcactctcgaagtgctgaagaagtaagagctccgggtt 1620
Db 1561 acttcgcgcagagacagcggaagcactctcgaagtgctgaagaagtaagagctccgggtt 1620
Qy 1621 aatgacacactgtgcaatgtgaaaggtgaaagaaatcaacacatgcccctgagacgcg 1680
Db 1621 aatgacacactgtgcaatgtgaaaggtgaaagaaatcaacacatgcccctgagacgcg 1680
Qy 1681 aatgctgcaacttgagagcactctccctggcgagagatcaaccacacacgtatgtgat 1740
Db 1681 aatgctgcaacttgagagcactctccctggcgagagatcaaccacacacgtatgtgat 1740
Qy 1741 cccgtcagctcgaatgtctggaagagagagagagagagagagagagagagagagagag 1800
Db 1741 cccgtcagctcgaatgtctggaagagagagagagagagagagagagagagagagagag 1800
Qy 1801 aagctgcatgagagagagagagagagagagagagagagagagagagagagagagagag 1860
Db 1801 aagctgcatgagagagagagagagagagagagagagagagagagagagagagagagag 1860
Qy 1861 ttctctgcaacactgtggaacatgactcccatgagacaaatgctcctggaagtggtg 1920
Db 1861 ttctctgcaacactgtggaacatgactcccatgagacaaatgctcctggaagtggtg 1920
Qy 1921 gaaacacatgttgagagctctcacaagagcccaaccagagatgagagagagagagagag 1980
Db 1921 gaaacacatgttgagagctctcacaagagcccaaccagagatgagagagagagagagag 1980
Qy 1981 tgaacacgctctcgaagcgcctgctggaagcactcctctccgagctcctcctccaca 2040
Db 1981 tgaacacgctctcgaagcgcctgctggaagcactcctcctccgagctcctcctccaca 2040

```

```

Qy 2041 gtcgtctctctcttgaggaaactcaactctctctctctctctccacaccccgctcactc 2100
Db 2041 gtcgtctctctcttgaggaaactcaactctctctctctctctccacaccccgctcactc 2100
Qy 2101 cccacactgacatgagcagatgagagagagagagagagagagagagagagagagagag 2160
Db 2101 cccacactgacatgagcagatgagagagagagagagagagagagagagagagagagag 2160
Qy 2161 tcggccacatgagagagagagagagagagagagagagagagagagagagagagagag 2196
Db 2161 tcggccacatgagagagagagagagagagagagagagagagagagagagagagag 2196

RESULT 10
ARI44956 2187 bp DNA Linear PAT 08-AUG-2001
LOCUS ARI44956 2187 bp DNA Linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6210950.
ACCESSION ARI44956
VERSION ARI44956.1 GI:15106823
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2187)
AUTHORS Johnson, W.G. and Stenroos, E.Scott.
TITLE Methods for diagnosing, preventing, and treating developmental disorders due to a combination of genetic and environmental factors
JOURNAL Patent: US 6210950-A 1 03-APR-2001;
FEATURES
source 1..2187
location/Qualifiers
BASE COUNT 479 a 655 c 616 g 437 t
ORIGIN

Query Match 99.2%; Score 2177.6; DB 6; Length 2187;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2180; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 10 gccatggtgaacgaagccagagagagagagagagagagagagagagagagagagagagag 69
Db 1 gccatggtgaacgaagccagagagagagagagagagagagagagagagagagagagagag 60
Qy 70 agcagtgagcagtgagagagagagagagagagagagagagagagagagagagagagag 129
Db 61 agcagtgagcagtgagagagagagagagagagagagagagagagagagagagagagag 120
Qy 130 gagcgcagatgagagagagagagagagagagagagagagagagagagagagagagag 189
Db 121 gagcgcagatgagagagagagagagagagagagagagagagagagagagagagagag 180
Qy 190 ttctccctggaatctctctccctcctcgaactgctgagagagagagagagagagagagag 249
Db 181 ttctccctggaatctctctccctcctcgaactgctgagagagagagagagagagagagag 240
Qy 250 ttgagcagatgagagagagagagagagagagagagagagagagagagagagagagag 309
Db 241 ttgagcagatgagagagagagagagagagagagagagagagagagagagagagagag 300
Qy 310 gaccctgagcacaagagagagagagagagagagagagagagagagagagagagagagag 369
Db 301 gaccctgagcacaagagagagagagagagagagagagagagagagagagagagagagag 360
Qy 370 tctgagcctgagagacacactctgacatgagagagagagagagagagagagagagagagag 429
Db 361 tctgagcctgagagacacactctgacatgagagagagagagagagagagagagagagagag 420
Qy 430 ggcacatctgacaaagctaaagcagctgagagagagagagagagagagagagagagagag 489
Db 421 ggcacatctgacaaagctaaagcagctgagagagagagagagagagagagagagagagag 480
Qy 490 ccaatagtgagcagagagagagagagagagagagagagagagagagagagagagagag 549

```











```

Db      781 GGTACACCTCCCTTGGGAGCTTGTGAACCTTCCAAAGCTGGAGGCGCCACAGGAGATC
Qy      853 aagaagctgattgagccaatcaagaacaagatgctgacatccgcaactatgcatgag
Db      841 AAGAGCTGATTAGCCCAATCAAGACAAAGACAGATGCTGCCATCCGCAACTATGGCATGAG
Qy      913 ctggcctgagcctgtgccaagagctcttgccagatgagcttgatgagccagcctccatc
Db      901 CTGGCCGTGAGCTGTGCCAGAGCTTCTTGCCAGTGGCTGGTGCCAGGCTCCACTTC
Qy      973 taacacctcaaccgagagatggtaccagagatgctgtgaagagcctggagatgagct
Db      961 TACACCTCAACCGCAGAGATGCTTACACAGAGTGTGAAGCGCTGGGAGATGTGACT
Qy      1033 gaagagcccaagagcgtccctaccctgcgtctcaagtgcaccccaagcgcgagagaa
Db      1021 GAGAGCCCCAGGCGTCCCTTACCCTGGGCTCTCAGTGCCACCCCAAGGCCGAGAGAA
Qy      1093 gatgatacctccatctcttgagcctccagacaagaagatatactacgtaaccagag
Db      1081 GATGATACGTCCCTTCTTGAGGCTCCAGACCAAGAGTACATCTACCTACCACAGAG
Qy      1153 tggagagagctccctcaacgagcgtggagagatccctcctccctgcttgaggagctg
Db      1141 TGGGAGAGATTCCTTAACGGCCCTGGGCAATTCCTTCCCTGCTTGGGAGACTG
Qy      1213 aagagtaactactcttctactaactgaagagcaagctccccaagagagagctgtaagatg
Db      1201 AAGAGTACTACTCTTCTTCTACCTGAAGAGCAAGTCCCCCAAGAGAGAGCTGTGAAGATG
Qy      1273 tgggaggagagagctgancgtgaagcaagtgcttngaagctttgtcttactctctg
Db      1261 TGGGGGAGAGAGCTGACCAATGAAGCAAGTGTGTAATCTTTGTCTTACCTCTCG
Qy      1333 gaggaaaccaaacggagatgctcaaaagtactgctgcctgcctggaacagatgagccctg
Db      1321 GAGAAACCAACCGGAGATGCTCAAAAGTACTTGCCTGCTGCGCTTGAACGATGAGCCCTG
Qy      1393 gggagctgaagacagcctgtctgaagagagagctgctcgagtgaaacgcgacagcctc
Db      1381 GCGGTGAGACCAAGCTGCTGAAGAGAGAGCTGCTGGGTGAACCGCAGGCGATCCTC
Qy      1453 accataactcacagcccaatcaacaggaagcgtctccgaccccatcgtggctg
Db      1441 ACCATTAACCTCACAGCCCAATCAACGGGAACCGCTCCCTCCACCCCATCTGGGCTGG
Qy      1513 ggcaccagcgaggctatgctctcagaagcgctactiaagtttcaactcccgag
Db      1501 GGCCTCAGGCGGGGCTATGCTTCCAGAAAGCCTTACTTACAGTTTTCACCTCCCGGAG
Qy      1573 acagggagagcactctctgcaagtgtctgaagaagtaacgagctccgggttaataccact
Db      1561 ACAGCGGAACCACTTCTGCAAGTGTGAAGAAAGTACGAGCTCCGGGTAAATTACACCTT
Qy      1633 gtcaatgtgaaggtgtaaaacatcaccaatgccccgaactgagccgaatggttact
Db      1621 GTCAATGTGAAGGTGTAATAACATCACCAATGCCCTGAACTGCAAGCCGATGCTGACT
Qy      1693 tgggagcattccctgagcgagagatcaccagcccaagctgaatgagctccgctcagctc
Db      1681 TGGGCGATCTTCCCTGGGAGAGATCATCACCCACCGCTAGTGTGATCCGTCAGCTTC
Qy      1753 atgtctggaagagagagccttgccttgctgtagatgagcggtggggaagctgtagag
Db      1741 ATGTTTGAAGAGACAGGCTTGGCTTGTGATTGAGCGGGGGAAGCGTATGAG
Qy      1813 gaagagatcccgctcccgcaacatcacatccagtagatcaacagacaactcctggtcaac
Db      1801 GAGGAGTCCCGCTCCGCAACATCATCATCATCAGACAACTACTTCTGCTGCTCAAC
Qy      1873 ctggtagacaatgactcccaactggaacaactgctctgcaagtggtggaagacacatg

```

```

Db      1861 CTGGTGACAAATGACTTCCACTGGACACTGCTCTGGCAGGTGTGAAGACACTTG
Qy      1933 gagcttccacaagagccaccagaatgagagaagaagagctccatga
Db      1921 GAGCTTCTCAACAGGCCCCACCAATGCGAGAAAGAGAGCGCTCATGA

```

```

RESULT 14
RNU57049      1250 bp  mRNA  linear  ROD 05-JUN-1996
LOCUS        Rattus norvegicus methylenetetrahydrofolate reductase mRNA, partial
DEFINITION
ACCESSION   cds.
VERSION     057049.1 GI:1354771
KEYWORDS
SOURCE      Rattus norvegicus strain-Wistar.
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1 (bases 1 to 1250)
AUTHORS    Li, Z., Chen, K.H., Zhang, C.H., Zhu, H.P., Meng, Z.H. and Tang, J.
TITLE      Direct Submission
JOURNAL    Submitted (29-APR-1996) J. Tang, The Institute of Cardiovascular
            Research, Beijing Medical University, Xue-Yuan Lu, Beijing, Beijing
            100083, P. R. China
FEATURES
            Location/Qualifiers
            source          1..1250
                        /organism="Rattus norvegicus"
                        /strain="Wistar"
                        /db_xref="taxon:10116"
                        /tissue_type="liver"
                        /dev_stage="adult"
                        /note="vector-pcEM-T; The cDNA was cloned by RT-PCR. The
                        two primers used in RT-PCR was designed based on the
                        sequence of human methylenetetrahydrofolate reductase"
                        <1..486
                        /product="methylenetetrahydrofolate reductase"
                        /protein_id="AB01988.1"
                        /db_xref="GI:1354772"
                        /translation="AMVNEARRGSPSPSEGRSGSESSKDSRSPSLPDRNER
                        LRKMRMRDSEDKWFLSPSPRGEGAFPTSGRTGMBGAPSPWMLPGVOVSMU
                        RGGDLITDKQHSHTLLMLGNPHADLLPAAREGDLRPPAQSQAARPEYNAENRPRC
                        R"

```

```

BASE COUNT      300 a      350 c      360 g      240 t
ORIGIN

```

```

Query Match      40.4%; Score 887.4; DB 10; Length 1250;
Best Local Similarity 83.8%; Pred. No. 1,4e-177;
Matches 1051; Conservative 0; Mismatches 197; Indels 6; Gaps 4;

```

```

Qy      10 gcatgtgtaagcaagcagagagaagacagcactcaaccctgctgagggcagtgc 69
Db      1 GCCATGCTGAACCAAGCAAGCAAGAGAGAGAGCCGCCCTTCTGAGGCTACA--- 57
Qy      70 aacagctggcagctgagagctccaaagatgctgagatgttccaccccgagctgaaacct 129
Db      58 AGAAGTGAAGTAGAGATGCTCAAGGACAGTTCAGATGTTCCACCCCAAGCTCGAGCCG 117
Qy      130 gaaagcatagagagactccggagaaagatagagcggagatgtaactctgtgcaagtgg 189
Db      118 GACCCGGAACGAGAGACTGCGGAGAGATGAGAGAAATVGAACCTTGAAAGCAAGTGG 177
Qy      190 ttctccctggaattctccctcctcgaactgctggaagagctgcaatcctcatcacaag 249
Db      178 TTCTCCCTGGAAGTCTCTCCCTCTCGAGAGAGAGAGACT-TTAACTCATCTGAGAG 236
Qy      250 tttagacgagatgacagagtgagcccccctcatatagaacgtgaccccaagcagt 309
Db      237 TTTGACCGGTTGGGGGAGGGGCCCTCTTGTGATGTACTGTGTAACCAAGAGTGAGC 296

```



QY	310	gccccttgcgaagcaaggagagactctccatctatgtagtcgcgaagcagccgctyaactac	369
Db	297	G-TCCTGGCTCAGCAAGAGACCTCTATCTATTAATTGGCACACAGCACTTAAGTAC	355
QY	370	ctatgacctggaagacacatctctgcacatctacgtctgcgcctcagcgcctggaaagatacag	429
Db	356	TGTCGCTTGGAAACCATCTCTGCACATGACCTGCTGCCAGACGGCCAGAGAGATCTCA	415
QY	430	ggcaatctgcgaagaagtaagcagctgagccttgaaagaaatcattgcgcctgcgagagagac	489
Db	416	GGCCACTGTGCACAGCCAGCCAGCAAGCTGGCTGTGAAGATTAATGAGGGCTGAGGGGAGAC	475
QY	490	ccaataagtgaccagtgaggaaagaaagaaagagagcttcaactacagcagtgagacatgtg	549
Db	476	CCGTAGTGCATCCACTGCGAAGCAGACGAGAGAGAGGCTTACGATATGGCACAGACTGTG	535
QY	550	aaagcaatccgaagtgatgatttgtagactcttgcacatctgtgtgcaagttaccccaa	609
Db	536	AAGCACTATCCGGAAACGATGTTGAGATTAATTTTGACATCTGTGTGGCAGGTTACCCCAA	595
QY	610	ggccaccgccgaagcaggagagcttllagagcctgcacctgcgaacacttgaaaggaaggttnt	669
Db	596	GGCCACCCCGATGACAGAGACTTCGAGGATGACCTGTAAGCACTGAAAGGAAGATTCAC	655
QY	670	ggagggagccgatctcatcatcaacgcagagcttctcttgaggctgcacatctctccgctt	729
Db	656	GCAAGGGCCGCACTTATCATCACTCAAGCTCTTTTGAGGGAGCGCTTCCTTCAGCTTC	715
QY	730	gtgaagagcatgcacgcagcatctggacatcacttgcacatctgcgcggagacttcccatc	789
Db	716	GTGAAGGCCGCGCAAGACATAGGCATCTCCTGCCATATCCTGGCTGGAGATCTTCCCTATC	775
QY	790	caaggttaccacactccctctggcagcgtcttfgaagcctgtccaagcttgaggtgcacaagag	849
Db	776	CAGGGCTTACACCTCCCTTGGCGCAGTTGTAAACTCTTCCAAAGCTGAGATCCACACAGACG	835
QY	850	atcaagagcgtgatitgagccaatcaagaacaaagcagctgcgcctcgcgaactctgtcatc	909
Db	836	ATCAAGATGTGTATGACGGCGATCAAAAGCAAGATGTGCCATCCGCCAACACGGCATT	885
QY	910	ggagctggccgttagcctgtgcgaagagcttctgcgcagttggttggatgcccagagcctccac	969
Db	896	GAGCTGTGTAACCTTGTGCCGGGAACGTGAGACAGTGGCTGTGGCGGGCGCTCCAC	955
QY	970	ttctacaacctcaaccgcgagatgtgctaccacaagag-gtctgaagcgcctggaggtatg	1028
Db	956	TTCACACTATCAACCGCAGGGGGGACCAATGAAAGTGTGAACCAACTGGCATGTG	1015
QY	1029	gactgagagaccccaagcgtctccctacactgcgctcagttgcccaccccaagcgcgagaa	1088
Db	1016	GACCAAGGACCCCAAGCGTCCTCCCTGCCCTGGCATGTGGCACCCCAAAAGCAGGGA	1075
QY	1089	gaaagaatgacgtcccatctctcttgagccctcgaagcaagaagagtatacatccgtaccca	1148
Db	1076	GGAAGTGTGGCTCCCATCTTGTGGGCCCTCAGACACCAAAAACTATATACCGCACACA	1135
QY	1149	ggagtgaggagagatctccctaacgcgcgcgtgggcaattctctccctgcctcttgggaa	1208
Db	1136	GGGCTGGGATGTGTTCCCAATGAGCGCGTGGGGTAAATCTTCTCAACCAAGCCTTGGGGA	1195
QY	1209	gctgaagagactacatcctcttacccttgaagaagaaagctccccaagagagagact	1262
Db	1196	GCTGAAGACTACTCTTCTTACTGAAAAGCAAGTCCCAAGGAGGAAGAACT	1249

RESULT	15
AF239166	AF239166 551 bp linear MM 08-MAY-2000
LOCUS	Sus scrofa methylenetetrahydrofolate reductase (MTHFR) mRNA,
DEFINITION	partial cds.
ACCESSION	AF239166
VERSION	AF239166.1 GI:7716550
KEYWORDS	.

SOURCE	pig.
ORGANISM	Sus scrofa
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
AUTHORS	1 (bases 1 to 551)
TITLE	Vallee,M., Pallin,M.-F.F., Guay,F., Beaudry,D., Blouin,R., Laforest,J.-P.P., Lessard,M. and Matte,J. Effect of folic acid supplement, breed and parity of sows on folate metabolism gene expression in early pregnancy
JOURNAL	unpublished
REFFERENCE	2 (bases 1 to 551)
AUTHORS	Vallee,M., Pallin,M.-F.F., Guay,F., Beaudry,D., Blouin,R., Laforest,J.-P.P., Lessard,M. and Matte,J.
TITLE	Direct Submission
JOURNAL	Submitted (25-FEB-2000) Agriculture and Agri-Food Canada Dairy and Swine Research and Development Centre, P.O. Box 90, 2000 Route 108 East, Lennoxville, Quebec J1M 1Z3, Canada
FEATURES	Location/Qualifiers
source	1..551
gene	/organism="Sus scrofa"
CDS	/strain="Breed Yorkshire-Landrace"
	/db_xref="taxon:9823"
	/dev_stage="embryo"
	<1..>.551
	/gene="MTHFR"
	<1..>.551
	/gene="MTHFR"
	/function="folate metabolism"
	/codon_start=3
	/product="methyltetrahydrofolate reductase"
	/protein_id="AF68431.1"
	/db_xref="GI:7716551"
	/translation="VIASTAVNYGLEYILHMTCCCHOSREEVTYGLHKARKLGLKNTILLRGGPVGDQWAEEGSGSYAADIYKHRSFGFYFDVCVAGYRGKPDHDESPADLRKHLKEVYAGDPIITOLFEEADTFPRFLAKASEMGITCPILPGIFIGIHSLSQLYVKLSKLEVPQOINDVIPERKDNNAA"
BASE COUNT	122 a 167 c 164 g 98 t
ORIGIN	
Query Match	20.4%; Score 447.6; DB 4; Length 551;
Best Local Similarity	88.2%; Pred. No. 1,8e+84;
Matches 486; Conservative	0; Mismatches 65; Indels 0; Gaps 0;
OY	341 tgatgatgcgcaagcaccgcgtgaactactgtgacctggagaacatccctgcacatgacct 400 
Db	1 TGTGATGCCCGACGACGCGCTGAACCTACTCGCGCTTGAGACCATGTCACATGACCT 60 
OY	401 gctgcgcgtcacgaccttgtagagatcacaggcgcatctgcasaagttagacgttggcc 460 
Db	61 GCTGCCATCAGACC CGGNGAGAGTCA CCGGCTTACTGCACAAGGCCAAGCGCTGGGCC 120 
OY	461 tgaagaacatcatgycgctgcggygagaaaccaatatgctgacagtgtaggaaagagaug 520 
Db	121 TGAAAAACATCTTGGCGCTGAGGGAGAACCTGTAGTGACAGTAGGGGAGACAGAGAG 180 
OY	521 gaagcttaacacagcagctgacacctgcytgaagacacatccgaagtgaattgttactact 580 
Db	161 GAAGCTTAAGCTACCTCAACCTTGATGGTAAGCACATCCGAGGAGATTGGTGTACTACT 240 
OY	581 ttgaacatctgttgcgcaagtttaccccagaagccccccaagcagagagagctttaagctg 640 
Db	241 TCGAGCTGTGTGTGGCAGGTTACCCCAAAGGCCAACCCGACGACAGAGAGCTTCAAGGCCG 300 
OY	641 accggaagcacttgaagagaagtgtnctcgggagccgaattcatcatcaacgagctt 700 
Db	301 ACCGTAAAACACTGAAAGAGAAGGTGGCGGACGAGAGCGCACTCATCATCAACCAAGCTTT 360 
OY	701 tccttgaagcgcagacacatcttcgcgttgttgaagagatgacagcaatggtgataact 760 
Db	361 TCCTTGAAGCGTGAATACGTTCTTCGCGCTTCTTGAAGGCTTGTGCTCCGAATATGAGATCACTT 420 
OY	761 gccccatgctcccgagatcttlcccatcagggctacacactcccttcggcagacttgta 820 



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 26, 2002, 15:37:08 ; Search time 338.85 Seconds  
(without alignments)  
11126.882 Million cell updates/sec

Title: SEQMOD  
Perfect score: 2196  
Sequence: 1 aatccgagccatgtgtgaa.....acctagctctctgtctcta 2196

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues  
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:\*  
5: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:\*  
6: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:\*  
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:\*  
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:\*  
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:\*  
10: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:\*  
11: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:\*  
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:\*  
13: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:\*  
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:\*  
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:\*  
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:\*  
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:\*  
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:\*  
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:\*  
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:\*  
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:\*  
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*  
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*  
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2186.6	99.6	2219	22	AAD20463 Human methylenetet
2	2186.6	99.6	2220	21	AAAS0633 Human methylenetet
3	2186.6	99.6	2230	22	AAD20462 Human methylenetet
4	2185	99.5	2219	17	AAT09689 Human methylene-te
5	2185	99.5	2220	17	AAT09694 Human methylene-te
6	2177.6	99.2	2187	22	AAC91206 Human methylenetet
7	1089.6	49.6	3283	21	AAAS0634 Mouse methylenetet
8	452.2	20.6	3181	21	AAAS0635 Human methylenetet
9	434.4	19.8	532	22	AAD20485 Human MTHFR gene e

c	10	434.4	19.8	23748	22	AA105229 Human reproductiv
	11	269.4	12.3	1942	21	AAC49168 Arabidopsis thalia
	12	255.4	11.6	341	22	AAD20479 Human MTHFR gene e
	13	250.8	11.4	1821	21	AAC43311 Arabidopsis thalia
	14	242	11.0	346	22	AAD20475 Human MTHFR gene e
	15	240.2	10.9	339	22	AAD20476 Human MTHFR gene e
	16	213.6	9.7	351	22	AAD20490 Mouse MTHFR gene e
	17	205.8	9.4	339	22	AAD20487 Mouse MTHFR gene e
	18	200.6	9.1	1335	21	AAC36967 Arabidopsis thalia
	19	200	9.1	294	22	AAD20478 Human MTHFR gene e
	20	184.8	8.4	281	22	AAD20481 Human MTHFR gene e
	21	184.8	8.4	283	22	AAD20482 Human MTHFR gene e
	22	181	8.2	343	22	AAD20486 Mouse MTHFR gene e
	23	172.8	7.9	1493	21	AAC44829 Arabidopsis thalia
	24	160	7.3	427	22	AAD20496 Mouse MTHFR gene e
	25	152.4	6.9	6727	24	AB133296 Human immune syste
	26	150.8	6.9	294	22	AAD20489 Mouse MTHFR gene e
	27	148	6.7	276	22	AAD20482 Mouse MTHFR gene e
	28	148	6.7	283	22	AAD20493 Mouse MTHFR gene e
	29	146	6.6	147	21	AA440624 Human MTHFR normal
	30	139.8	6.4	235	22	AAD20480 Human MTHFR gene e
	31	135	6.1	6727	24	AB133297 Human immune syste
	32	130	5.9	144	21	AA440625 Human MTHFR HC fra
	33	124.2	5.7	220	22	AAD20484 Human MTHFR gene e
	34	120	5.5	235	22	AAD20491 Mouse MTHFR gene e
	35	119	5.4	120	22	AAD11821 Methylenetetrahydr
	36	115.2	5.2	210	22	AAD20477 Human MTHFR gene e
	37	114.8	5.2	558	21	AA250061 Soybean 5,10-methy
	38	106.2	4.8	202	22	AAD20483 Human MTHFR gene e
	39	99.6	4.5	219	22	AAD20495 Mouse MTHFR gene e
	40	91.4	4.2	876	24	AA597261 Mouse MTHFR gene e
	41	88.6	4.0	211	22	AAD20488 Mouse MTHFR gene e
	42	81.8	3.7	349980	21	AAF21609 Neisseria meningit
	43	79	3.6	80	22	AAH02417 Human MTHFR coding
	44	77.4	3.5	80	22	AAH02418 Human MTHFR coding
	45	74.6	3.4	759	21	AAA81845 N. meningitidis pa

## ALIGNMENTS

RESULT	1
ID	AAD20463 standard; cDNA; 2219 BP.
XX	XX
AC	AAD20463:
XX	XX
DT	03-JAN-2002 (first entry)
XX	XX
DE	Human methylenetetrahydrofolate reductase (MTHFR) protein cDNA #2.
KW	Human; methylenetetrahydrofolate reductase; MTHFR; gene therapy; glioma; antilease therapy; EC 1.5.1.20; chromosome 1p36.3; cancer; kidney cell;
KW	pancreas; lung; brain; cytosolic; colon carcinoma; breast; colorectal;
KW	neuroblastoma; leukaemia; ss.
XX	XX
OS	Homo sapiens.
XX	XX
FH	Key
FT	CDS
FT	13..1983
FT	/*tag- a
FT	/product- "Human methylenetetrahydrofolate reductase
FT	(MTHFR) protein"
FT	/EC_number- "1.5.1.20"
XX	XX
PN	US2001025030-A1.
XX	XX
PD	27-SEP-2001.
XX	XX
PF	01-DEC-2000; 2000US-0728910.
XX	XX
PR	01-MAR-1999; 99US-0258928.
XX	XX

PA (ROZE/) ROZEN R.  
PA (SEKH/) SEKHON J.

XX Rozen R, Sekhon J;

DR WPI: 2001-638509/73.

PI P-PSDB: AAE12607.

XX New antisense nucleic acids, which are methylenetetrahydrofolate  
PT reductase inhibitors, useful for treating, stabilizing or preventing  
PT cancer, e.g. breast carcinoma, colon carcinoma, colorectal carcinoma or  
PI neuroblastoma

XX Disclosure: Fig 6; 68pp; English.

CC The invention relates to a non allele-specific antisense nucleic acids,  
CC which binds to methylenetetrahydrofolate reductase (MTHFR: EC 1.5.1.20)  
CC nucleic acids and inhibits MTHFR protein expression in a mammal. MTHFR  
CC catalyses the NADPH-linked reduction of 5,10-methylenetetrahydrofolate to  
CC 5-methylenetetrahydrofolate, a co-substrate for methylation of  
CC homocysteine to methionine. The invention provides potential therapy for  
CC individuals with MTHFR deficiency. The non allele-specific antisense  
CC nucleic acids are useful for treating, stabilizing or preventing cancer,  
CC particularly breast carcinoma, colon carcinoma, colorectal carcinoma,  
CC lung cancer, brain cancer, pancreatic cancer, kidney cell cancer,  
CC neuroblastoma, glioma and leukemia. MTHFR cDNA probe is used in gene  
CC therapy. The present sequence is human methylenetetrahydrofolate  
CC reductase (MTHFR) protein cDNA #2. Human MTHFR gene is mapped to  
CC chromosome 1p36.3.

SQ Sequence 2219 BP; 501 A; 657 C; 620 G; 441 T; 0 other;

Query Match 99.6%; Score 2186.6; DB 22; Length 2219;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

OY 1 aattccggagccatggtgagcgaagcaagaaagacagctcacaacccctgctggag 60
DB 1 aattccggagccatggtgagcgaagcaagcaagaaagacagctcacaacccctgctggag 60
OY 61 ggcagctgcagcagctgagcagtgagcgtccaaagatgctcgagatgtccaccccgag 120
DB 61 ggcagctgcagcagctgagcagtgagcgtccaaagatgctcgagatgtccaccccgag 120
OY 121 ctggagccctgagcagcagtgagcagcgtcggaagagatgagcgcgcatgtgaatctggt 180
DB 121 ctggagccctgagcagcagtgagcagcgtcggaagagatgagcgcgcatgtgaatctggt 180
OY 181 gacaagtggtctccctggaattcttcctcctcgaaactgctgagggagactgtcaatttc 240
DB 181 gacaagtggtctccctggaattcttcctcctcgaaactgctgagggagactgtcaatttc 240
OY 241 atctcaaggttgaccgagatgagcagcaggtggtccctctacatagacgtgacccgagac 300
DB 241 atctcaaggttgaccgagatgagcagcaggtggtccctctacatagacgtgacccgagac 300
OY 301 ccagagagtgagcctcgctcagacagaagagacactctctcattatgatactgcagcacgc 360
DB 301 ccagagagtgagcctcgctcagacagaagagacactctctcattatgatactgcagcacgc 360
OY 361 gtagaactctgtgctcgagagacacatctctgacatgacactgtgctgcgtcaagcgccctggag 420
DB 361 gtagaactctgtgctcgagagacacatctctgacatgacactgtgctgcgtcaagcgccctggag 420
OY 421 gagatcacgggcatctgcacaaagctaaagcagctggccttgaggaatacatctgctgctg 480
DB 421 gagatcacgggcatctgcacaaagctaaagcagctggccttgaggaatacatctgctgctg 480
OY 481 cgggagagacccaatagtgagcagtgaggaagagagagagagagagagagagagagagagag 540
DB 481 cgggagagacccaatagtgagcagtgaggaagagagagagagagagagagagagagagagag 540

```

```

OY 541 gacctgtgaagcacatcccgaaagtgaattgtgtactactttgacatctgtgtgcaggt 600
DB 541 gacctgtgaagcacatcccgaaagtgaattgtgtactactttgacatctgtgtgcaggt 600
OY 601 taccacaagagccaccccgaaagcagggagctttgaggtgaactgaagcaacttgaagag 660
DB 601 taccacaagagccaccccgaaagcagggagctttgaggtgaactgaagcaacttgaagag 660
OY 661 aaggtgtgctggagagcagcttcatcatcagcagagctttctttgaggtgacacatc 720
DB 661 aaggtgtgctggagagcagcttcatcatcagcagagctttctttgaggtgacacatc 720
OY 721 ttccgcttgtagaagcagtcacccagacatgagcatcacttgcaccatcgtcccgagatc 780
DB 721 ttccgcttgtagaagcagtcacccagacatgagcatcacttgcaccatcgtcccgagatc 780
OY 781 ttcccatccagggctacacccctcctcctcgcaagctttagaagctgtccaagctggaagtg 840
DB 781 ttcccatccagggctacacccctcctcctcgcaagctttagaagctgtccaagctggaagtg 840
OY 841 ccacagagatcacaagcagtgatgagccaatcaacaagacagatgtgcacatccgcaac 900
DB 841 ccacagagatcacaagcagtgatgagccaatcaacaagacagatgtgcacatccgcaac 900
OY 901 tatgcatcagagctggccgtgagcctgtgccaagagcttctggccaagtgtgtgtgcca 960
DB 901 tatgcatcagagctggccgtgagcctgtgccaagagcttctggccaagtgtgtgtgcca 960
OY 961 ggcctcactcttaccacccctcacaaccccgagatgagcttaccacaagagtgcttgaagcgctg 1020
DB 961 ggcctcactcttaccacccctcacaaccccgagatgagcttaccacaagagtgcttgaagcgctg 1020
OY 1021 gggatgtgacttgaagaccccaagcgctccctcctcctgctcctacagtcccccacag 1080
DB 1021 gggatgtgacttgaagaccccaagcgctccctcctcctgctcctacagtcccccacag 1080
OY 1081 cgcgagagagaaagtatgaagctccatcttctggcctcagacaaagagttacatctac 1140
DB 1081 cgcgagagagaaagtatgaagctccatcttctggcctcagacaaagagttacatctac 1140
OY 1141 cgtaccagaagatggagacagatccctcaacggcgctgaggaatccctcctccctgac 1200
DB 1141 cgtaccagaagatggagacagatccctcaacggcgctgaggaatccctcctccctgac 1200
OY 1201 ttggggagctggaagactactactctcttctacatcttgaagaagcagctccccaagagagag 1260
DB 1201 ttggggagctggaagactactactctcttctacatcttgaagaagcagctccccaagagagag 1260
OY 1261 ctgctgaaagatgtggggagagagagcctgancagtgaaagcagtgctcttgaagtctt 1320
DB 1261 ctgctgaaagatgtggggagagagagcctgancagtgaaagcagtgctcttgaagtctt 1320
OY 1321 cttacactctcggaagaaacaaacccggaatgtgtcacaagaagtgaactgtgctgcctggaa 1380
DB 1321 cttacactctcggaagaaacaaacccggaatgtgtcacaagaagtgaactgtgctgcctggaa 1380
OY 1381 gatgaagccctggcggtgagacccagcctgtctgaagagagagctgctgggtgaaacgc 1440
DB 1381 gatgaagccctggcggtgagacccagcctgtctgaagagagagctgctgggtgaaacgc 1440
OY 1441 cagggcatctcctacatcaatcaacacagcccaacatcaagggagacgctctccgaaccc 1500
DB 1441 cagggcatctcctacatcaatcaacacagcccaacatcaagggagacgctctccgaaccc 1500
OY 1501 atcgtggctgtggcccgagcggtgtgtcttccagaagagcctacttaagttttc 1560
DB 1501 atcgtggctgtggcccgagcggtgtgtcttccagaagagcctacttaagttttc 1560
OY 1561 acttcgcgagacagcgggaagcacttctgcagagtgtctgaagaagttaagagctccgggtt 1620
DB 1561 acttcgcgagacagcgggaagcacttctgcagagtgtctgaagaagttaagagctccgggtt 1620
OY 1621 aattacacactgtctcaatgtgaaagtgaaaaacatcaacacatgcccctgaaactgcagcgg 1680

```

Db	1621	aattacaacctgttcaatgtgaaaggtgtaaacataccaatgtcccttgaacttcagagcgt	1680
Qy	1681	aatgtctcaacttggggacatcttcctctgggcgagagatcatccaagccaccgtatggat	1740
Db	1681	aatgtctcaacttggggacatcttcctctgggcgagagatcatccaagccaccgtatggat	1740
Qy	1741	ccgttcagcttcatgttctctggaaagacagagccttgccttcgcttgaattgacgggtggga	1800
Db	1741	ccgttcagcttcatgttctctggaaagacagagccttgccttcgcttgaattgacgggtggga	1800
Qy	1801	aagctgatgagagagaggtcccccgtcccgacacatcatccaatlacatccacgacaattac	1860
Db	1801	aagctgatgagagagaggtcccccgtcccgacacatcatccaatlacatccacgacaattac	1860
Qy	1861	tctcctgttcaaaccttgatgagacaattgacctcccaactcgtgcagactcctctgtcgaggtgtg	1920
Db	1861	tctcctgttcaaaccttgatgagacaattgacctcccaactcgtgcagactcctctgtcgaggtgtg	1920
Qy	1921	gaagacacatattgagagcttctccaacagcccaacccaagaatctgcgagagaaacgagagctcca	1980
Db	1921	gaagacacatattgagagcttctccaacagcccaacccaagaatctgcgagagaaacgagagctcca	1980
Qy	1981	tgacctctgcctctcagcgccttcgcttgtagagccaactctctgtcccgcttctctctccaca	2040
Db	1981	tgacctctgcctctcagcgccttcgcttgtagagccaactctctgtcccgcttctctctccaca	2040
Qy	2041	gtgcctgtctctcttgggaactccactctctctgtgtctctccacaccccgagctccactc	2100
Db	2041	gtgcctgtctctcttgggaactccactctctctgtgtctctccacaccccgagctccactc	2100
Qy	2101	ccccacactgacaacatgagcagactctagacttgagatgagagcttccagagcttcttcctggacctgag	2160
Db	2101	ccccacactgacaacatgagcagactctagacttgagatgagagcttccagagcttcttcctggacctgag	2160
Qy	2161	tcggccccacatgagggaacctgaacttactctctgcctcta	2196
Db	2161	tcggccccacatgagggaacctgaacttactctctgcctcta	2196
RESULT 2			
AAA50633			
ID	AAA50633 standard; cDNA; 2220 BP.		
XX			
AC	AAA50633;		
XX			
DT	19-DEC-2000 (first entry)		
XX			
DE	Human methylentetrahydrofolate reductase cDNA.		
XX			
KX	Methylenetetrahydrofolate reductase: MTHFR; human; folic acid;		
KW	cardiovascular disorder; cancer; neuroblastoma;		
KW	colorectal carcinoma; osteoporosis; neural tube		
KW	neurological disorder; gene therapy; diagnosis; chromosome 1p36.3;		
KW	ss.		
OS	Homo sapiens.		
XX			
FH	Key		
FT	CDS		
FT	Location/Qualifiers		
FT	13..1983		
FT	/*tag- a		
FT	/EC.number="1.5.1.20"		
FT	replace(167,A)		
FT	mutation		
FT	/*tag- b		
FT	replace(402,A)		
FT	/*tag- c		
FT	mutation		
FT	/*tag- d		
FT	replace(559,T)		
FT	/*tag- e		
FT	mutation		
FT	/*tag- f		
FT	replace(677,T)		
FT	/*tag- g		
FT	mutation		
FT	/*tag- h		
FT	replace(692,T)		
FT	/*tag- i		
FT	mutation		
FT	/*tag- j		
FT	replace(764,T)		

FT	mutation	/*tag- 9	replace(792+1,A)
FT		/*tag- h	replace(985,T)
FT	mutation	/*tag- i	replace(1015,T)
FT	mutation	/*tag- j	replace(1018,T)
FT	mutation	/*tag- k	replace(1298,C)
FT	mutation	/*tag- l	replace(1317,C)
FT	mutation	/*tag- m	
PN			MO200052205-A2.
XX			
XX			08-SEP-2000.
PD			
XX			28-FEB-2000; 2000MO-IB00442.
PF			
XX			01-MAR-1999; 99US-0258928.
PR			
XX			(UYMC-) UNIV MCGILL.
PA			
XX			Rozen R, Goyette P;
P1			
DR			WPI: 2000-572192/53.
DR			P-PSDB: AAY96186.
XX			
XX			CDNA probe for the human methylenetetrahydrofolate reductase (MTHFR),
PT			useful in gene therapy and for diagnosing or treating MTHFR deficiency
PT			which is associated with cardiovascular disorders or cancer
XX			
PS			Claim 1; Fig 1A-F; 93pp; English.
XX			
CC			The present sequence is that of cDNA coding for human
CC			methylenetetrahydrofolate reductase (MTHFR, see AAY96186), an enzyme
CC			catalysing the NADPH-linked reduction of 5,10-methylenetetrahydrofolate
CC			to 5-methyltetrahydrofolate, a co-substrate for methylation of
CC			homocysteine to methionine. To identify human MTHFR cDNA, PCR
CC			primers based on the porcine sequence were used to screen a human
CC			liver lambda-gt10 cDNA library by PCR. A 1266 bp fragment was
CC			obtained, and this was used to screen a human colon carcinoma cDNA
CC			library to obtain the 2.2 kb clone. The MTHFR gene (see AAY50634)
CC			maps to chromosome 1p36.6. A cDNA probe for human MTHFR, which
CC			hybridises to the present sequence, is claimed. This probe can be
CC			used to identify MTHFR sequence abnormalities in individuals with
CC			severe or mild MTHFR deficiency. These abnormalities may comprise
CC			a mutation selected from 167G to A, 482G to A, 559C to T, 677C to
CC			T, 692C to T, 764C to T, 792+1G to A, 985C to T, 1015C to T, 1081C
CC			to T, 1298A to C and 1317T to C. MTHFR deficiency may be associated
CC			with a cardiovascular disorder, cancer (especially neuroblastoma or
CC			colorectal carcinoma), osteoporosis, neural tube defect in an
CC			offspring of a patient, neurological disorders, and other disorders
CC			influenced by folic acid metabolism. Also claimed are methods for
CC			treating MTHFR deficiency by gene therapy or by administration of
CC			MTHFR protein. Cancer can be treated by inhibiting MTHFR gene
CC			expression or MTHFR protein activity, or by administering an agent
CC			that modifies MTHFR gene expression.
XX			
XX			Sequence 2220 BP; 501 A; 658 C; 620 G; 441 T; 0 other;
XX			
Query Match	99.6%	Score 2186.6;	DB 21; Length 2220;
Best Local Similarity	99.7%	Pred. No. 0;	
Matches 2189;	Conservative 0;	Mismatches 7;	Indels 0; Gaps 0;
Qy	1	aattccgagccatggtgtaacgaagcagaaggaagaagcagcctcaaccctgtcttgag	60
Db	1	aattccgagccatggtgtaacgaagcagaaggaagaagcagcctcaaccctgtcttgag	60
Qy	61	ggcagtgccagcagtggtgcaagtggaagctccaaagatagttcgaagatgttccacccgggc	120

[illegible]

OY	1201	tttgggagctgaaagcactactactctcttcttcaacttgaaagcgaagctcccccagagagag	1260
Db	1201	tttgggagcctgaaagaaactaactactcttcttcaacttgaaagcgaagctcccccagagagag	1260
OY	1261	ctgcgcgaagatgttgggggagagactgacnccagctgaagcaaatgtctcttngaagctcttgct	1320
Db	1261	ctgcgcgaagaaagtgtgggggagagagctgacnccagctgaagcaaatgtctcttngaagctcttgct	1320
OY	1321	ctttaacctctcgaggagaaaccaaacccggaatggttcaacaagtgtactgtctctgcgccccttgaaac	1380
Db	1321	ctttaacctctcgaggagaaaccaaacccggaatggttcaacaagtgtactgtctctgcgccccttgaaac	1380
OY	1381	gatggagcccccggcgcgctcgagaaacaaagccctgtctgaaagagagagctgcgtcgcggttgaaacgcgc	1440
Db	1381	gatggagcccccggcgcgctcgagaaacaaagccctgtctgaaagagagagctgcgtcgcggttgaaacgcgc	1440
OY	1441	caggagcatctctcaaccaatcaactacacagccaaacatacaagggaaagccgctctccgaaacccc	1500
Db	1441	caggagcatctctcaaccaatcaactacacagccaaacatacaagggaaagccgctctccgaaacccc	1500
OY	1501	atcgtaggcctctggggcccccagcgcggtgactatgtcttccagaagctcacttgaagtttttc	1560
Db	1501	atcgtaggcctctggggcccccagcgcggtgactatgtcttccagaagctcacttgaagtttttc	1560
OY	1561	acttcccgcgagaaacagcgaaagcactctctcgaaagtgtctgaagaagtacgaagcttcgggtt	1620
Db	1561	acttcccgcgagaaacagcgaaagcactctctcgaaagtgtctgaagaagtacgaagcttcgggtt	1620
OY	1621	aattacacacctgttcaaatgtgaaggtgtgaaaaacatcaacaatgcccccttgaaacttcgaacgcg	1680
Db	1621	aattacacacctgttcaaatgtgaaggtgtgaaaaacatcaacaatgcccccttgaaacttcgaacgcg	1680
OY	1681	aatgtctgtcaactttggggcactcttcccctggcgagagatcatctcaagcccaacgcgtatgtgat	1740
Db	1681	aatgtctgtcaactttggggcactcttcccctggcgagagatcatctcaagcccaacgcgtatgtgat	1740
OY	1741	cccggtcaacacttcaatgtcttctggaagaaacgaagccctttgcctgtgaattgagcggttgaggga	1800
Db	1741	cccggtcaacacttcaatgtcttctggaagaaacgaagccctttgcctgtgaattgagcggttgaggga	1800
OY	1801	aagctgtatagagagagatcccccgttcccgcacaacatcatcatgaatcatctcaacgacaactaac	1860
Db	1801	aagctgtatagagagagatcccccgttcccgcacaacatcatcatgaatcatctcaacgacaactaac	1860
OY	1861	tccctgttcaaaccttgtagaacaatgaatcttcccaacttgagacaactgcctcttgacaggtgtg	1920
Db	1861	tccctgttcaaaccttgtagaacaatgaatcttcccaacttgagacaactgcctcttgacaggtgtg	1920
OY	1921	gaagaacacatgtgagacttcttcaacaagcccaacccaagaatgcgagagaaacgagagcttcca	1980
Db	1921	gaagaacacatgtgagacttcttcaacaagcccaacccaagaatgcgagagaaacgagagcttcca	1980
OY	1981	tgaacctgtgtctactaagcccccgtgttgtagagcaatctctgtcccgcccttctctctccaca	2040
Db	1981	tgaacctgtgtctactaagcccccgtgttgtagagcaatctctgtctcccgcccttctctctccaca	2040
OY	2041	ggtcgtctctctcttgtagaactccaactctctctgtctctcccaaccccggtctccacatc	2100
Db	2041	ggtcgtctctctcttgtagaactccaactctctctgtctctcccaaccccggtctccacatc	2100
OY	2101	cccccaactgacaacatgacgactgagatgtgaagcttccaggtctctctctgagacgtgag	2160
Db	2101	cccccaactgacaacatgacgactgagatgtgaagcttccaggtctctctctgagacgtgag	2160
OY	2161	tcggccccacatgtagaacctagttactctctgtctca	2196
Db	2161	tcggccccacatgtagaacctagttactctctgtctca	2196
RESULT 3			
AAD20462 standard: cDNA: 2220 BP			

RESULT	3
AAD20462	
ID	AAD20462 standard; cDNA; 2220 BP.

Key	Location/Qualifiers
Key	1.1983
CDS	/*tag= a
FT	/product= "Human methylenetetrahydrofolate reductase
FT	(MTHFR) protein"
FT	/note= "CDS does not include start codon"
FT	/EC.number= "1.5.1.20"
FT	/partial
XX	US2001025030-A1.
XX	27-SEP-2001.
XX	01-DEC-2000; 2000US-0728910.
XX	01-MAR-1999; 99US-0258928.
XX	(ROZE/) ROZEN R.
XX	(SEKH/) SEKHON J.
XX	Rozen R, Sekhon J;
XX	WPI, 2001-638509/73.
XX	P-PSDB; AAEL12606.
XX	New antisense nucleic acids, which are methylenetetrahydrofolate
XX	reductase inhibitors, useful for treating, stabilizing or preventing
XX	cancer, e.g. breast carcinoma, colon carcinoma, colorectal carcinoma or
XX	neuroblastoma
XX	Disclosure: Fig 1; 68pp; English.
XX	The invention relates to a non allele-specific antisense nucleic acids,
XX	which binds to methylenetetrahydrofolate reductase (MTHFR; EC 1.5.1.20)
XX	nucleic acids and inhibits MTHFR protein expression in a mammal. MTHFR
XX	catalyses the NADPH-linked reduction of 5,10-methylenetetrahydrofolate to
XX	5-methylenetetrahydrofolate, a co-substrate for methylation of
XX	homocysteine to methionine. The invention provides potential therapy for
XX	individuals with MTHFR deficiency. The non allele-specific antisense
XX	nucleic acids are useful for treating, stabilizing or preventing cancer,
XX	particularly breast carcinoma, colon carcinoma, colorectal carcinoma,
XX	lung cancer, brain cancer, pancreatic cancer, kidney cell cancer,
XX	neuroblastoma, glioma and leukemia. MTHFR cDNA probe is used in gene
XX	therapy. The present sequence is human methylenetetrahydrofolate
XX	reductase (MTHFR) protein cDNA #1. Human MTHFR gene is mapped to
XX	chromosome 1p36.3.
XX	Sequence 2220 BP; 501 A; 658 C; 620 G; 441 T; 0 other;
XX	Query Match 99.6%; Score 2186.6; DB 22; Length 2220;
XX	Best Local Similarity 99.7%; Pred. No. 0;
XX	Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX	1 aattccgagcagcatgtttaaagcaagccagagaagcaagcagcctcaacccctgttgag 60
XX	
XX	1 aattccgagcagcatgtttaaagcaagccagagaagcaagcagcctcaacccctgttgag 60
XX	
XX	61 ggcagtcgcagcagtcgagtcgagcctccaagaatagtcgagatgttccaccgcgagc 120

[illegible]



```

Db 1141 cgtaccaggagtggaacagatgcccttaacgcccgtggtggcaattcctctccctgcc 1200
OY 1201 ttctggagagctgaagactactactctctctactctgaagaagcccccaaggagagag 1260
Db 1201 ttctggagagctgaagactactactctctctactctgaagaagcccccaaggagagag 1260
OY 1261 ctgtctaaagatgtgggggggagagctgancagatgaagcaagtgctttnaagcttctgt 1320
Db 1261 ctgtctaaagatgtgggggggagagctgancagatgaagcaagtgctttnaagcttctgt 1320
OY 1321 ctctactctctcgagaaacaaacacggaatgtcacaaagtgtactgtccctgtgaaac 1380
Db 1321 ctctactctctcgagaaacaaacacggaatgtcacaaagtgtactgtccctgtgaaac 1380
OY 1381 gatgagccctgtgagctgtgagaccagctgtctgaagagagagtgctgtgggtgaaaccc 1440
Db 1381 gatgagccctgtgagctgtgagaccagctgtctgaagagagagtgctgtgggtgaaaccc 1440
OY 1441 caggagcatcctccacatcaactcaacagcccaacatcaacagcgagagcgtctccgaccc 1500
Db 1441 caggagcatcctccacatcaactcaacagcccaacatcaacagcgagagcgtctccgaccc 1500
OY 1501 atcgtgggtctgggccccagcggggtatgtcttcagaaggctacttagagtttttc 1560
Db 1501 atcgtgggtctgggccccagcggggtatgtcttcagaaggctacttagagtttttc 1560
OY 1561 actcccgcgagagacagcgagacactctgtcaagtgtctgaagaagtacgagctccgggtt 1620
Db 1561 actcccgcgagagacagcgagacactctgtcaagtgtctgaagaagtacgagctccgggtt 1620
OY 1621 aattaccacttgcatactgtgaagggttgaacaatcaacatgcacatgccttgaaactgcagcg 1680
Db 1621 aattaccacttgcatactgtgaagggttgaacaatcaacatgcacatgccttgaaactgcagcg 1680
OY 1681 aatgtctgaacttgggggcatctccctcgggcgagagatcatccagcccgacgagtgat 1740
Db 1681 aatgtctgaacttgggggcatctccctcgggcgagagatcatccagcccgacgagtgat 1740
OY 1741 cccgtcagctcatgtctctggaagacgagccttgcctgtagattgagcggtggga 1800
Db 1741 cccgtcagctcatgtctctggaagacgagccttgcctgtagattgagcggtggga 1800
OY 1801 aagctgtatgagagagaggtcccgctccgacacatcatccagatcacatccagacaaactac 1860
Db 1801 aagctgtatgagagagaggtcccgctccgacacatcatccagatcacatccagacaaactac 1860
OY 1861 ttccgtgtcaacactgtgtgacaatgacttcccaactggaacactgtcctgtgaggtgtg 1920
Db 1861 ttccgtgtcaacactgtgtgacaatgacttcccaactggaacactgtcctgtgaggtgtg 1920
OY 1921 gaagaacacattggagcttctcaacagcccaacgaatgcgagagaagagaggtctcca 1980
Db 1921 gaagaacacattggagcttctcaacagcccaacgaatgcgagagaagagaggtctcca 1980
OY 1981 tgaccgcgtctcgtgaagcctcgtgttggagccactcctctcccgctctcctccaca 2040
Db 1981 tgaccgcgtctcgtgaagcctcgtgttggagccactcctctcccgctctcctccaca 2040
OY 2041 gtgtctgtctctcttggaaactcaactcctctcgtgtctctcccaaccgggctccaactc 2100
Db 2041 gtgtctgtctctcttggaaactcaactcctctcgtgtctctcccaaccgggctccaactc 2100
OY 2101 ccccaactggaacatggcagctagaactgaggtgaagcttccagagcttctcctgagacctgag 2160
Db 2101 ccccaactggaacatggcagctagaactgaggtgaagcttccagagcttctcctgagacctgag 2160
OY 2161 tcggcccaacatgggaacctagtaactctctgctcta 2196
Db 2161 tcggcccaacatgggaacctagtaactctctgctcta 2196

```

RESULT 4  
AAT09689

```

ID AAT09689 standard; cDNA: 2219 BP.
AC AAT09689;
XX 15-OCT-1996 (first entry)
DT 15-OCT-1996 (first entry)
XX 15-OCT-1996 (first entry)
DE Human methylene-tetrahydrofolate-reductase cDNA.
XX Methylene-tetrahydrofolate-reductase; MTHFR; gene therapy;
KM cardiovascular disease; neurological disease; folic acid metabolism;
KW EC-1.5.1.20; enzyme: ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH CDS 13..1980
FT /tag= a
FT
XX W09533054-A1.
XX 07-DEC-1995.
XX 25-MAY-1995; 95WO-CA00314.
XX 26-MAY-1994; 94GB-0010620.
XX (UVMC-) UNIV MCGILL.
XX Goyette P, Rozen R;
XX WPI: 1996-030565/03.
XX P-PSDB: AAR8358.
XX Human methylene-tetrahydrofolate reductase cDNA probe - for
PT detection of sequence abnormalities in methylene-tetrahydrofolate
PT reduction e.g. in cardiovascular, neurological or folic acid
PT metabolism disorders
XX PS Disclosure: Fig. 6A-6C; 66pp; English.
XX CC This sequence encoding human MTHFR has been localised to chromosome
CC 1p36.3. It may be used for the construction of DNA probes which may
CC be used for the identification of sequence abnormalities in patients
CC with severe or mild MTHFR deficiency. The resulting probe may also
CC be used in gene therapy to produce the MTHFR protein.
XX CC
XX Sequence 2219 BP; 501 A; 656 C; 620 G; 442 T; 0 other;
SQ

```

Query Match 99.5%; Score 2185; DB 17; Length 2219;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 2188; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

OY 1 aattccggagccatggtgacgaagccagagaaacagagctcaacccctgtgag 60
Db 1 aattccggagccatggtgacgaagccagagaaacagagctcaacccctgtgag 60
OY 61 ggcagtgccagcagctgagcagtgagctccaagaatgttgagatgttccaccccggtc 120
Db 61 ggcagtgccagcagctgagcagtgagctccaagaatgttgagatgttccaccccggtc 120
OY 121 ctgagaccctgagcagcatagagaccccggaagaatgagcggcgatgtgaatctggt 180
Db 121 ctgagaccctgagcagcatagagaccccggaagaatgagcggcgatgtgaatctggt 180
OY 181 gacaagtgttctcctctggaatcttccctcctcgaaactgcgagggagctgtcaatctc 240
Db 181 gacaagtgttctcctctggaatcttccctcctcgaaactgcgagggagctgtcaatctc 240
OY 241 atctcaagtttgaccgggttgagcaggttgagccctctacaataacgtgaccgtgac 300
Db 241 atctcaagtttgaccgggttgagcaggttgagccctctacaataacgtgaccgtgac 300

```









	Query Match	49.6%	Score 1089, 6	DB 21	Length 3283	
	Best Local Similarity	68.6%	Pred. No. 3e-243			
	Matches 2181	Conservative	0	Mismatches	7	Indels 989; Gaps 10
CC	offspring of a patient. neurological disorders, and other disorders					
CC	influenced by folic acid metabolism. Also claimed are methods for					
CC	treating MTHFR deficiency by gene therapy or by administration of					
CC	MTHFR protein. Cancer can be treated by inhibiting MTHFR gene					
CC	expression or MTHFR protein activity, or by administering an agent					
CC	that modifies MTHFR gene expression. Isolation of the human MTHFR					
CC	gene forms part of an effort to study MTHFR deficiency in					
CC	homocystinuria and in multifactorial diseases.					
XX						
SQ	Sequence 3283 BP; 664 A; 1001 C; 951 G; 667 T; 0 other;					
QY	9 agacatgtgtgaacgaaagcagagagaaacagacagcctcaacccctctgtgaagcgacgtgc					68
DB	57 agccatgtgtgaacgaaagcagagagaaacagacagcctcaacccctctgtgaagcgacgtgc					116
QY	69 cagcagctgacgtgagaagctccaaagatgtgtcgaagatgttccaccccgagccttgagacc					128
DB	117 cagcagctgacgtgagaagctccaaagatgtgtcgaagatgttccaccccgagccttgagacc					176
QY	129 tgaagcgacatgaagagacctccgagagagatgaagtcgagctggaatctgtgtgacaagtgc					188
DB	177 tgaagcgacatgaagagacctccgagagagatgaagtcgagctggaatctgtgtgacaagtgc					236
QY	189 gtctccctccggaaatttctccctccctctgaaactgtctgagagagctgtcaatctcaatc--					246
DB	237 gtctccctccggaaatttctccctccctccctgaaactgtctgagagagctgtcaatctcaatc					296
QY	247 -----					246
DB	297 gtaactcatgacaagttaagtgtagagagcgaggatgtgtgctctgagagcagatgtgata					356
QY	247 -----					246
DB	357 ttctctctggaacctctctctcaagaaacaaacccctcaagatcttgacgagatgacgag					416
QY	269 gtggcccccctctacatagacgtgacactgagccacagatgtgacccctgtgtccagacaag					328
DB	417 gtggcccccctctacatagacgtgacactgagccacagatgtgacccctgtgtccagacaag					476
QY	329 agacctctccatgatgatgtatctgcagacacgcgcgtgaaactactctgtgctctggaacatcc					388
DB	477 agacctctccatgatgatgtatctgcagacacgcgcgtgaaactactctgtgctctggaacatcc					536
QY	389 tgcacatgaaactgtgtgcctgcacagagcctctgagagagatcaacagcgccactctccacaaga					448
DB	537 tgcacatgaaactgtgtgcctgcacagagcctctgagagagatcaacagcgccactctccacaaga					596
QY	449 agcagctgagcgctgagagaaacatactgagcgtctgggg-----					485
DB	597 agcagctgagcgctgagagaaacatactgagcgtctgggg-----					656
QY	486 -----					485
DB	657 acactctggtgtctcgcttctcccggaagcctctgtaggtgtgtgtgagaccgaatgataatg					716
QY	486 -----					486
DB	717 acctccacaacacctgacagcccaatagtgtagccaggtggaagagagagagagaggttc					776
QY	529 aactacgacagtgagcctgtgtgaagcacacatccggaagtgaattgtgtgtgactacttgaacatc					588
DB	777 aactacgacagtgagcctgtgtgaagcacacatccggaagtgaattgtgtgtgactacttgaacatc					836
QY	589 tttgt-----					592
DB	837 tgtgtgacaggtgagtgctgctgcatcatcctgtgtgtgagagatgaagctaaagaggtctgac					896
QY	593 -----					593





```

OY 2080 ctccaccgagctcactccaccactgacaatgcaagtgaagtgaagcttc 2139
DB 3117 ctccaccgagctcactccaccactgacaatgcaagtgaagtgaagcttc 3176
OY 2140 cagctctctctgactgagtcgcccacatggagacactgactctgctcta 2196
DB 3177 cagctctctctgactgagtcgcccacatggagacactgactctgctcta 3233

RESULT 8
ID AAA50635 standard; DNA; 3181 BP.
XX
XX AAA50635;
AC
XX 19-DEC-2000 (first entry)
DT
XX
XX Mouse methylentetrahydrofolate reductase gene.
DE
XX
XX Methylentetrahydrofolate reductase; MTHFR; mouse; gene therapy;
KW diagnosis; chromosome 4; ds.
XX
XX Mus musculus.
OS
XX
XX Key
FH 61..3020
FT CDS
FT
FT Location/Qualifiers
FT
FT /tag= a
FT /note= "contains introns"
FT
FT /tag= b
FT /number= 1
FT
FT /tag= c
FT /number= 1
FT
FT /tag= d
FT /number= 2
FT
FT /tag= e
FT /number= 2
FT
FT /tag= f
FT /number= 3
FT
FT /tag= g
FT /number= 3
FT
FT /tag= h
FT /number= 4
FT
FT /tag= i
FT /number= 4
FT
FT /tag= j
FT /number= 5
FT
FT /tag= k
FT /number= 5
FT
FT /tag= l
FT /number= 6
FT
FT /tag= m
FT /number= 6
FT
FT /tag= n
FT /number= 6
FT
FT /tag= o
FT /number= 7
FT
FT /tag= p
FT /number= 7
FT
FT /tag= p

```

```

FT /number= 8
FT 2283..2382
FT /tag= q
FT /number= 8
FT 2383..2484
FT /tag= r
FT /number= 9
FT 2485..2585
FT /tag= s
FT /number= 9
FT 2586..2705
FT /tag= t
FT /number= 10
FT 2706..2804
FT /tag= u
FT /number= 10
FT 2805..3020
FT /tag= v
FT /number= 11

```

W0200052205-A2.

08-SEP-2000.

28-FEB-2000; 2000MO-IB00442.

01-MAR-1999; 99US-0258928.

(UYMC-) UNIV MCGILL.

Rozen R, Goyette P;

WPI; 2000-572192/53.

CDNA probe for the human methylentetrahydrofolate reductase (MTHFR), useful in gene therapy and for diagnosing or treating MTHFR deficiency which is associated with cardiovascular disorders or cancer -

Disclosure; Fig 13A-B; 93pp; English.

The present sequence is that of the mouse gene encoding CC methylentetrahydrofolate reductase (MTHFR), an enzyme catalyzing CC the NADPH-linked reduction of 5,10-methylentetrahydrofolate CC to 5-methyltetrahydrofolate, a co-substrate for methylation of CC homocysteine to methionine. The gene maps to distal chromosome 4. CC The mouse MTHFR gene is very similar in size and structure to the CC human MTHFR gene (see AAA50634). Mouse MTHFR genomic clones may be CC used to make constructs for gene targeting and generation of mouse CC models for MTHFR deficiency, which in humans is associated with CC cardiovascular disorders, cancer, osteoporosis and neurological CC disorders.

Sequence 3181 BP; 712 A; 912 C; 916 G; 641 T; 0 other;

Query Match 20.6%; Score 452.2; DB 21; Length 3181;

Best Local Similarity 60.1%; Pred. No. 3.1e-95; Mismatches 196; Indels 698; Gaps 8;

Matches 1346; Conservative 0; Mismatches 196; Indels 698; Gaps 8;

```

OY 9 agccatggtgaacgaaagcagagaaacagcctcaaccctgctgagggcagtc 68
DB 57 agccatggtgaacgaaagcagagaaagcagcctcaaccctgctgagggcag--- 113
OY 69 cagcagtgagtgagagctccaaagatgctcagagatgtccacccgggctgagacc 128
DB 114 cagcagtgagtgagagctccaaagatgctcagagatgtccacccgggctgagacc 173
OY 129 tgagcgagtgagagctccggagagatgagcgagcttggaatctgtgacaagtg 188
DB 174 agagcgagtgagagctccggagagatgagcgagcttggaatctgtgacaagtg 233
OY 189 gtctccctggaattctccctcctcgaaactgctgagggagctgcatcatcctc--- 245

```

Db 234 gtctccctggaagtctctcccccctcgaaactgctgagggagctgttaacctatctccag 293  
OY 246 ----- 245  
Db 294 gttgagtagggaggttaatccgcggggtctgcgaggtcttaaggggagcggtgagctcccta 353  
OY 246 -----aaagtttgaacggatgagcag 268  
Db 354 tttaaccacgagagcctaacttaaggagaatccctacaggttttgaacggatgagcag 413  
OY 269 gtggccccctcctacataagacgtgaccttggaaccacgacgggtgacacctgtgttaagacaag 328  
Db 414 gggggccccctcctcgtataatgttacctgacccacgctgagagacctgtgtcagaagaag 473  
OY 329 agaacctctcctacatgatactgcgcacgacgcgctgtaaactactgtgtgccccgagacatcc 388  
Db 474 agacctccctcctatgtatctgcgcacgacagacagataactactgcggtcttggaacaacctatc 533  
OY 389 tgcataatgacctgtgcgctcagcgctgagagagatcaacgggacatctgcaacaagcta 448  
Db 534 tgcataatgacctgtgcgctcagcgcccgagagagatcaacgacatctgcaacagagcca 593  
OY 449 agcacctgagccctgaggaacatcatctggcgctgcgggg----- 485  
Db 594 agcacctgagccctgaggaacatcatctggcgctgcggggagaggtgtgcgcgcagcacccctcc 653  
OY 486 ----- 485  
Db 654 tctttgggtctctgtcttccctgaaggcttcttgaggtctcaaggcgacacccagtgacatg 713  
OY 486 -----agaccaataagtgacacagtgaggaaaggagaaaggagcttc 528  
Db 714 acctccagcaacctgcgcacaccttgtaagtgacacatctgggaagcagagaaaggagagcttc 773  
OY 529 aactcagcagtgagacctgtgtgaagacacatccgaaagtgaagttgtgtgactactgtacatc 588  
Db 774 agctatgtcacaaagacactgtgtgaagacacatccgaaagttgtgtgactatatttgacatc 833  
OY 589 tctgtgac----- 596  
Db 834 tgtgtgagagtgtaagtgagagacagaaaggttcaagatgagagagtaagccagctagctt 893  
OY 597 -----aggttaacccaa 608  
Db 894 gcaagtgagttgagagacgacccctactctctgtctcctcctgtaaggttaacccag 953  
OY 609 aggcacaccccgaaagcagagagcttgaagctgagcctgaaagcacttgaaaggagaaagtgtn 668  
Db 954 aggcacaccccgatgagagagcttgcgagatgagcctgaaagcattgaaaggagaaagttatc 1013  
OY 669 tgcggagacgcatctcatcatcaacgacagcttcttgaagcctgaacacattctccgct 728  
Db 1014 tgcaggcgcgacactcatcatcactcagctctcttcttgaaggcagacacattctcagct 1073  
OY 729 tgtgaagcagtcagccacgacatctgagcacttgccccctgccccggagatcttccat 788  
Db 1074 tgtgaagcagtcagccacgacatctcctctgcacctacccctgcggagcttcccat 1133  
OY 789 ----- 788  
Db 1134 tcaagtgaggggttgaggagacactgattccctccgtccagtgcatgaggaagtcagtg 1193  
OY 789 -----ccagggtaccacatcccttc 808  
Db 1194 agcatagggcagagatgaccccatgccccctgtgtctctgacaggtacacatcccttc 1253  
OY 809 ggcagctgtgaagcgtgtccaaagcttgaggtgacacagaaatacaagacgtgattgagc 868  
Db 1254 ggcagctgtgaagcgtgtccaaagcttgaggtgacacagaaatacaagacgtgattgagc 1313  
OY 869 caatcaagaagacacgagtgtgcacatccgcaactatgcatcagactggtgcgtgagcgtgt 928  
Db 1314 ccatcaagaagacacgagtgtgcacatccgcaactagcgcatgagctgtgctgtaagcgctgt 1373

OY 929 gccaaagactctggccaaatggcttggtgcacaggcctccactctacacccctcaacgcg 988  
Db 1374 gccgggagctgtgtgaacagtgctgtgtgcacaggcctccactctacacccctcaacgcg 1433  
OY 989 agatggtctacacaaaggtgtctgaagcgcttggggagtgtgactgaagac----- 1039  
Db 1434 aggtggtccacatgagaggtgtctaaagcaacttggcatgtgagccgagacccagtgag 1493  
OY 1040 ----- 1039  
Db 1494 cgggtgaaagctgagagacataccatgagtcaagatctgcgacaggtgactagctaccc 1553  
OY 1040 -----ccaggcgctccctacacctgcgtctcagt 1068  
Db 1554 taagccctgtcttcttccctctctctctccctcctcaagcgctcccttgccctggtctcagt 1613  
OY 1069 gcccaaccccaagcgccgagagaaagatgtaagctcccatctctgtggcctcagaccaaag 1128  
Db 1614 gcgcatacccaagcgccgagagaaagatgtaagctcccatctctgtggcctcagaccaaag 1673  
OY 1129 agttacatctaccgtacccagagagtgaggacaggttccctaaagcgct----- 1177  
Db 1674 agctacatctaccgtacccagagagtgaggacaggttccctaaagcgcttgtagagagag 1733  
OY 1178 ----- 1177  
Db 1734 aagcaggggggtgttagaattgctgtgctggtgtggaataatagagaaatttaaacac 1793  
OY 1178 -----ggggcaattcctcttccctgcttgaggga 1208  
Db 1794 aaagtcctgttcccttactactcctgcgcagggtgaattcttctcacaacgcttgaggga 1853  
OY 1209 gctgaaggaactactcctcttactctgaaggaaggtcccccagggagagcgtgtgtaa 1268  
Db 1854 gctgaaggaactactcctcttactcctgaaggaaggtcccccagggagagcgtgtgtaa 1913  
OY 1269 gatgtgggggagagagctgaaacagtgaaagcagtgctcttngaaagtctgttcttactc 1328  
Db 1914 gatgtggggcgagagagctcaacagcgaagagagtgctcttngaaagtctgttcttactc 1973  
OY 1329 ctggggaagacaaacggaaatgtgtcacaaagt----- 1362  
Db 1974 ctctggagagccgaatctgcacatggtcactacagatgtggtgtgagaggaagccacagc 2033  
OY 1363 ----- 1362  
Db 2034 ttgtgtcagccttgccccaggtcccaagactcagtgctgcctcgtctcagcgacacctgc 2093  
OY 1363 -----acttgctgccttggaacgatgagccctggtgcgtgtgaagacagcgtgtg 1413  
Db 2094 ctgcaggtacacctgctgcctcggaacgatgaaacccctgcgcgggaacacagcctgatg 2153  
OY 1414 aagggagagcgtgtgcgtgtgaacgcgacagggcatctcaacatcaactcaagcccaac 1473  
Db 2154 aagggagagcgtgtgcgtgtgaacaggtgtggtgcacatccacatcaactcaagcccaac 2213  
OY 1474 atcaacgggaagcgctcctccgaacccatctgtggtgtggggcccaagggggtatgtc 1533  
Db 2214 atcaacgggaagcgctcctccgaacccatctgtgtggtgtggggcccaagggggtatgtc 2273  
OY 1534 ttccagaagcgctactaga 1553  
Db 2274 ttccagaagcgctactaga 2293

RESULT 9  
AAD20485  
ID AAD20485 standard; DNA; 532 BP.  
XX  
AC AAD20485;  
XX  
DT 03-JAN-2002 (first entry)

Db	99	gagggagctcccgctcccgagaccatcatcatcagtaacatccagaaacatacttccgtgtcaac	158
Qy	1873	ctggtgtgagcaatgacttccactcagtcagaaactgtcctctgtgcaggctgtgtgaaagacacatg	1932
Db	159	cttggtgtgagcaatgacttccactcagtcagaaactgtcctctgtgcaggctgtgtgaaagacacatg	218
Qy	1933	gagcttcccaacagagccaccacagaaatgcgagagagaaacggagagctcatataccctgtcgtc	1992
Db	219	gagcttcccaacagagccaccacagaaatgcgagagagaaacggagagctcatataccctgtcgtc	278
Qy	1993	ctgagccctcgtcgtgtgagagcaactctgtcccgccctcctcctccacagtgctgtcttc	2052
Db	279	ctgagccctcgtcgtgtgagagcaactctgtcccgccctcctcctccacagtgctgtcttc	338
Qy	2053	ttgggaactccactctctctgtgtgtctctccacacccggcctccacttccccacactgaca	2112
Db	339	ttgggaactccactctctctgtgtgtctctccacacccggcctccacttccccacactgaca	398
Qy	2113	atgagagctagactcgtgagtgaggttccaggtcttctctcctgagacttgagtcggccacacat	2172
Db	399	atgagagctagactcgtgagtgaggttccaggtcttctctcctgagacttgagtcggccacacat	458
Qy	2173	gggaacctagactctctctgtcctca	2196
Db	459	gggaacctagactctctctgtcctca	482
RESULT 10			
AAL05229/c			
ID	AAL05229	standard; DNA; 23748 BP.	
XX	XX		
AC	AAL05229;		
XX	XX		
DT	21-NOV-2001	(first entry)	
XX	XX		
DE	Human reproductive system related antigen DNA SEQ ID NO: 7917.		
KW	Human; reproductive system related antigen; reproductive system disorder		
KW	cancer; gene therapy; ds.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
PN	MO200155320-A2.		
XX	XX		
PD	02-AUG-2001.		
XX	XX		
FE	17-JAN-2001;	2001WO-US01339.	
XX	XX		
PR	31-JAN-2000;	2000US-0179065.	
PR	04-FEB-2000;	2000US-0180628.	
PR	24-FEB-2000;	2000US-0184564.	
PR	02-MAR-2000;	2000US-0186350.	
PR	16-MAR-2000;	2000US-0189874.	
PR	17-MAR-2000;	2000US-0190076.	
PR	18-APR-2000;	2000US-0198123.	
PR	19-MAY-2000;	2000US-0205515.	
PR	07-JUN-2000;	2000US-0209467.	
PR	28-JUN-2000;	2000US-0214886.	
PR	30-JUN-2000;	2000US-0215135.	
PR	07-JUL-2000;	2000US-0216647.	
PR	07-JUL-2000;	2000US-0216880.	
PR	11-JUL-2000;	2000US-0217487.	
PR	11-JUL-2000;	2000US-0217496.	
PR	14-JUL-2000;	2000US-0218290.	
PR	26-JUL-2000;	2000US-0220963.	
PR	26-JUL-2000;	2000US-0220964.	
PR	14-AUG-2000;	2000US-0224518.	
PR	14-AUG-2000;	2000US-0224519.	
PR	14-AUG-2000;	2000US-0225213.	
PR	14-AUG-2000;	2000US-0225214.	
PR	14-AUG-2000;	2000US-0225266.	
PR	14-AUG-2000;	2000US-0225267.	
PR	14-AUG-2000;	2000US-0225268.	



Db 8558 CTGATGACATATGACTTCCCACTGGACAACTGCCTCTGGCAGGTGTTGAAGACATATG 8499  
QY 1933 gagcttcaacagagcccccagaatgcagagaaacgagagctcatcaccctgcgtc 1992  
Db 8498 GAGCTTCTCAACAGGCCCCACCAGAAATGCGAAGAAAGGAGGCTTCATGACCTGGCTC 8439  
QY 1993 ctgacgcccgcgtctggagcaccctcgtccgcgcctctctctccacagatgctcttc 2052  
Db 8438 CTGACGCCCTTCGTTGAGACCACTCCTGTCTCCGCCCTTCTCCTCCTCAAGTCTCTTC 8379  
QY 2053 ttgggaactcactctcctctgtctctctccaccgcgcctcactcccccactgaca 2112  
Db 8378 TTGGGAACCTCAGCTCTCTCTGTCTCTCCACCCCGGCTCCACTCCACCTGACA 8319  
QY 2113 atggcaactgactgagtgtaggttccaggtcttctctgagactgtagtggcccaat 2172  
Db 8318 ATGGCACTGACTGAGTGAAGGCTTCCAGGCTTCTTCTGACCTGAGTGGGCCCACT 8259  
QY 2173 gggaaactagtaactctctgctcta 2196  
Db 8258 GGGAACTAGTACTCTGTGCTTA 8235

## RESULT 11

AAC49168

ID AAC49168 standard; DNA; 1942 BP.

XX AAC49168:

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 60181.

XX Hybridisation assay: genetic mapping; gene expression control;

KM protein identification; signal transduction pathway;

KM metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 04-MAY-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0139119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144884.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145085.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145219.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145813.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.

```

PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148319.
PR 13-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 16-AUG-1999; 99US-0148684.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155139.
PR 24-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155559.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159741.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.

```

```

PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 12.3%; Score 269.4; DB 21; Length 1942;
Best Local Similarity 51.2%; Pred. No. 7.7e-53;
Matches 909; Conservative 0; Mismatches 789; Indels 78; Gaps 9;

QY 151 gagaagatgagcgcgatggagatctgtgagacaagtggtctccctggaattctccct 210
DB 13 gataagatccagcattatagcgcgaaggaagaacagcggttctccctggaattctccca 72
QY 211 cctcgaaatgctgaggaagctgtcaatctcatcctaaggtttgacccgagtgcaagagt 270
DB 73 ccaagaagacaagatgagtgacgaatctcttgagagatgagatcgaatggtgtctat 132
QY 271 ggcacctcaataagacgtgacgtgaccccaagcgagtgaccctggtcagacaagag 330
DB 133 ggtcaacggtttgcgatatcacttgg-----ggagctggtggtatcaccgca 180
QY 331 acctcccatgatatcgccagcagccggtgaactactgtggtcgtgagacaatcctg 390
DB 181 gatctaagcttgatatactgctcgagatgacaacggttgtgtgtgagagatgagt 240
QY 391 ccaatgacctgctgcgtcagcgcctgagaggaatcagcgagccatctcacaagaagtaag 450
DB 241 catctacgtgtactaactgctgctgtgagagatgatactgctgtgagatatataga 300
QY 451 cagctgagcctgaggaacatcatgagcgtgctgaggaagccaataggt-----gaccag 504
DB 301 tctaattgagattcagaatgtgtgtctctctagaggtgagtgatctccctcagtgcaagataag 360
QY 505 tgggaagagaggaaggaagcctcaactagcagtgagcctggtggaagacacatccgaagt 564
DB 361 ttgttcaggttggaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 420
QY 565 gaggttgtgactactgtgacatctgtgtgagaggttaaccacaagggccaccccgag-- 622
DB 421 aaglatgtgtactactgtgtgatactgtgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 480
QY 623 -----caggagccttgaagcctgagcctggaacattggaag 657
DB 481 attgtgaggaatggtctgctgctcaatgaagctatagaagtgatgtgtgtgtgtgtgtgt 540
QY 658 gagaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 717
DB 541 aaaaagattgagcgtgagcgtgactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
QY 718 ttcttcgcttgtgagagcgtgacacgacatggtgacatctggtcccatcgtcccgagg 777
DB 601 ttcttcaggttgtgagagatgtgtgcgcaaatgtgaggttgaaggtgtgtgtgtgtgtgt 660
QY 778 atcttcccatccaggggtacacactccctcggcagagtttgaagctgtgcacagcgtgag 837
DB 661 attatgcttataataactacagaggttttgcgtatgactgtgtgtgtgtgtgtgtgtgtgt 720
QY 838 gtgccaagagagatcaagagcgtgattgagccaatacaagaacagatgtgtgtgtgtgtgt 897
DB 721 ataccagtgagagtgagtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 780
QY 898 aactatgagcatcgagctgagcgtgagcgtgtgagcagagctgtgtgtgtgtgtgtgtgt 957
DB 781 gctatgtgattacacttggaacagagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 840
QY 958 ccaagcctcacttcaacccctcaacgcgagagatgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1017
DB 841 tc-----tcttcatctcacaatggaacatgaggaatctgtgtgtgtgtgtgtgtgtgtgt 897
QY 1018 ctggagatgtgactgagagcccaag--ggttccctcaactcgtgtgtgtgtgtgtgtgtgtgt 1074

```

Db	898	cttgcgtatgattgtagtgcgaataatttccttcgttcttaccctgcggaaagccctgcgaat	957		
Qy	1075	cccaagccgcgagagagagatgtaacgtcccatctcttcggccctccagaacaaagttaac	1134		
Db	958	gtttccgtactaaaggagatgtgcgcccattctctggtgcnaaacgctccaaagagctac	1017		
Qy	1135	attcacgctaccgagaggttggaaagatttcctcaacggccgcttggggcaattctcttc	1194		
Db	1018	attctaaagaacaaaggccctggaaagattcccaacaaggccgggtgggttatcagcagt	1077		
Qy	1195	ccctgccttggggagcctgnaagaaatacctcttccatccttgaagagcaagtcgcccaag	1254		
Db	1078	gtctcaatagttgcacctcctgcgatacagttcttcacgtcccg-----cgagcacgtgac	1131		
Qy	1255	gagagagctgcgtgaagatgctgggggggaaagctgmcnctgtaagaaagtgtccttngaagtc	1314		
Db	1132	aagaagcttcaacaagaatggtgtgtcccatctgnaaaggtgttgaagaattatccagaa	1191		
Qy	1315	ttctgtcttcaacctctcgggagaaaccaacggagatgttcaacaagtgatctgcctcc	1374		
Db	1192	tccaagagagcctctgccttgcgaaccttaaaagc-----agtcctgtgtctgaat	1240		
Qy	1375	tggaaagatgaagccctctggcgctgtgaacacagcctctgaagagagagcctgtgcgggtg	1434		
Db	1241	tagatgga-----ctccagccgagaaacaagataataaaccgagcaatctgataaagctc	1293		
Qy	1435	aaccgcgagggcctatcccaacatactcaacgaagcccaacatcaacgggaagccgtctcc	1494		
Db	1294	aactccaagaagctctcttgcacataaataagccaacatcagttcaacgcccggagagatcgtat	1353		
Qy	1495	gaacccacgtgtggccttgggcccacagcgggggctatgtcttccagaagagcctactagag	1554		
Db	1354	tcaccaactgtgtgagtgagggcctcgttggatagtataccaaagagcttatctagag	1413		
Qy	1555	ttttcaacttccgcgcggagacgcggaaagcactcttgcgaagtgcctgaagaagtacagctc	1614		
Db	1414	tctctctgcgtccaagaggaataatagatgcagtggttggagaaatgcaagctt---gcca	1470		
Qy	1615	cgggttlaattaccacacttgtcaatgtgaaggttgaaaaacatcaccaatgcctctgaactg	1674		
Db	1471	tcgattacttaccatgtgcgtgtgaacaagaagaaacagtggtatctgaacacttgcaccaagct	1530		
Qy	1675	cagccgaatgtctgtcaacttcttgggggcatcttcccttggcggagagatcatccagccacgta	1734		
Db	1531	gatgtgaatgtctgttaacttcttggggagtttcccggtctaaggaaatcatcttcaaccaacatt	1590		
Qy	1735	gtggtatccgcgaactcatatcttcttggaaagacgaagccttgcgcctgtgatgtgacgg	1794		
Db	1591	gtcgtatcccgctagctcttcaacgctcttggagaagatgaagcatttggacttgttcaagaagc	1650		
Qy	1795	tggggaaagctgtatagaggaagatcccgctccgcgaacatcatcagtaatcatccagac	1854		
Db	1651	tgggtctaactgtttaccagaagcgcgaaccccttccagaacattgtctcggaggttgaagaac	1710		
Qy	1855	aactacttccctgtcacaacttgttgaacatgagctc	1890		
Db	1711	agctactattgttgaagctgtgttggaaacagattac	1746		
RESULT 12					
ID	AAD20479	standard; DNA; 341 BP.			
AC	AAD20479;				
XX	03-JAN-2002	(first entry)			
DE	Human MTHFR gene exon 5 with partial intron sequence.				
XX					
KW	Human: methyltetrahydrofolate reductase; MTHFR; gene therapy; glioma; antisense therapy; EC 1.5.1.20; chromosome 1p36.3; cancer; kidney cell; pancreas; lung; brain; cytosolic; colon carcinoma; breast; colorectal; neuroblastoma; leukemia; ds.				
KW					



[illegible]

RESULT 13

AAC43311  
JD AAC43311 standard; DNA; 1821 BP.

AC AAC43311;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38803.

KW Hybridisation assay; genetic mapping; gene expression control,  
 KW protein identification; signal transduction pathway;  
 KW metabolic pathway; promoter; termination sequence; ss.  
 YY

05 *Arabidopsis thaliana*.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR	05-FEB-1999	9905-0121823
PR	05-MAR-1999	9905-0123180
PR	09-MAR-1999	9905-0123548
PR	23-MAR-1999	9905-0125788
PR	25-MAR-1999	9905-0126564
PR	29-MAR-1999	9905-0126785
PR	01-APR-1999	9905-0127462
PR	06-APR-1999	9905-0128234
PR	08-APR-1999	9905-0128734
PR	16-APR-1999	9905-0128645
PR	19-APR-1999	9905-0128645
PR	21-APR-1999	9905-0130077
PR	23-APR-1999	9905-0130449
PR	23-APR-1999	9905-0130510
PR	28-APR-1999	9905-0130891
PR	30-APR-1999	9905-0131448
PR	30-APR-1999	9905-0133048
PR	04-MAY-1999	9905-0132407
PR	04-MAY-1999	9905-0132484
PR	05-MAY-1999	9905-0132485
PR	06-MAY-1999	9905-0132485
PR	06-MAY-1999	9905-0132487
PR	07-MAY-1999	9905-0132487
PR	11-MAY-1999	9905-0133863
PR	14-MAY-1999	9905-0134256
PR	14-MAY-1999	9905-0134218
PR	14-MAY-1999	9905-0134219
PR	14-MAY-1999	9905-0134321
PR	14-MAY-1999	9905-0134370
PR	18-MAY-1999	9905-0134376
PR	18-MAY-1999	9905-0134768
PR	20-MAY-1999	9905-0134494
PR	21-MAY-1999	9905-0135124
PR	24-MAY-1999	9905-0135353
PR	25-MAY-1999	9905-0135629
PR	27-MAY-1999	9905-0136031
PR	28-MAY-1999	9905-0136392
PR	01-JUN-1999	9905-0136782
PR	01-JUN-1999	9905-0137232
PR	03-JUN-1999	9905-0137558
PR	04-JUN-1999	9905-0137562
PR	07-JUN-1999	9905-0137724
PR	08-JUN-1999	9905-0137724
PR	10-JUN-1999	9905-0138094
PR	10-JUN-1999	9905-0138540
PR	10-JUN-1999	9905-0138847
PR	14-JUN-1999	9905-0139119

PR	16-JUN-1999;	9905-0139452
PR	16-JUN-1999;	9905-0139453
PR	17-JUN-1999;	9905-0139492
PR	18-JUN-1999;	9905-0139454
PR	18-JUN-1999;	9905-0139455
PR	18-JUN-1999;	9905-0139456
PR	18-JUN-1999;	9905-0139457
PR	18-JUN-1999;	9905-0139458
PR	18-JUN-1999;	9905-0139459
PR	18-JUN-1999;	9905-0139460
PR	18-JUN-1999;	9905-0139461
PR	18-JUN-1999;	9905-0139462
PR	23-JUN-1999;	9905-0140354
PR	23-JUN-1999;	9905-0140355
PR	24-JUN-1999;	9905-0140356
PR	24-JUN-1999;	9905-0140695
PR	25-JUN-1999;	9905-0140823
PR	30-JUN-1999;	9905-0140991
PR	01-JUL-1999;	9905-0141287
PR	01-JUL-1999;	9905-0141842
PR	02-JUL-1999;	9905-0142154
PR	02-JUL-1999;	9905-0142055
PR	06-JUL-1999;	9905-0142390
PR	08-JUL-1999;	9905-0142803
PR	09-JUL-1999;	9905-0142920
PR	12-JUL-1999;	9905-0142977
PR	13-JUL-1999;	9905-0143542
PR	14-JUL-1999;	9905-0143624
PR	15-JUL-1999;	9905-0144005
PR	16-JUL-1999;	9905-0144088
PR	19-JUL-1999;	9905-0144088
PR	19-JUL-1999;	9905-0144325
PR	19-JUL-1999;	9905-0144331
PR	19-JUL-1999;	9905-0144332
PR	19-JUL-1999;	9905-0144333
PR	19-JUL-1999;	9905-0144334
PR	20-JUL-1999;	9905-0144335
PR	20-JUL-1999;	9905-0144352
PR	20-JUL-1999;	9905-0144632
PR	21-JUL-1999;	9905-0144884
PR	21-JUL-1999;	9905-0144884
PR	21-JUL-1999;	9905-0145086
PR	22-JUL-1999;	9905-0145088
PR	22-JUL-1999;	9905-0145085
PR	22-JUL-1999;	9905-0145087
PR	22-JUL-1999;	9905-0145089
PR	22-JUL-1999;	9905-0145192
PR	23-JUL-1999;	9905-0145145
PR	23-JUL-1999;	9905-0145218
PR	26-JUL-1999;	9905-0145224
PR	27-JUL-1999;	9905-0145276
PR	27-JUL-1999;	9905-0145513
PR	27-JUL-1999;	9905-0145518
PR	28-JUL-1999;	9905-0145519
PR	28-JUL-1999;	9905-0145521
PR	02-AUG-1999;	9905-0146586
PR	02-AUG-1999;	9905-0146588
PR	02-AUG-1999;	9905-0146589
PR	03-AUG-1999;	9905-0147038
PR	04-AUG-1999;	9905-0147038
PR	04-AUG-1999;	9905-0147204
PR	05-AUG-1999;	9905-0147192
PR	05-AUG-1999;	9905-0147192
PR	06-AUG-1999;	9905-0147260
PR	06-AUG-1999;	9905-0147303
PR	06-AUG-1999;	9905-0147416
PR	09-AUG-1999;	9905-0147493
PR	09-AUG-1999;	9905-0147935
PR	11-AUG-1999;	9905-0148171
PR	11-AUG-1999;	9905-0148319

```

PR 12-AUG-1999; 990S-0148341.
PR 13-AUG-1999; 990S-0148565.
PR 13-AUG-1999; 990S-0148684.
PR 16-AUG-1999; 990S-0149368.
PR 17-AUG-1999; 990S-0149175.
PR 18-AUG-1999; 990S-0149426.
PR 20-AUG-1999; 990S-0149722.
PR 20-AUG-1999; 990S-0149723.
PR 20-AUG-1999; 990S-0149929.
PR 23-AUG-1999; 990S-0149902.
PR 23-AUG-1999; 990S-0149930.
PR 25-AUG-1999; 990S-0150566.
PR 26-AUG-1999; 990S-0150884.
PR 27-AUG-1999; 990S-0151065.
PR 27-AUG-1999; 990S-0151066.
PR 30-AUG-1999; 990S-0151080.
PR 31-AUG-1999; 990S-0151303.
PR 01-SEP-1999; 990S-0151438.
PR 01-SEP-1999; 990S-0151930.
PR 07-SEP-1999; 990S-0152363.
PR 10-SEP-1999; 990S-0153070.
PR 13-SEP-1999; 990S-0153758.
PR 15-SEP-1999; 990S-0154018.
PR 16-SEP-1999; 990S-0154039.
PR 20-SEP-1999; 990S-0154779.
PR 22-SEP-1999; 990S-0155139.
PR 23-SEP-1999; 990S-0155486.
PR 24-SEP-1999; 990S-0155659.
PR 28-SEP-1999; 990S-0156458.
PR 29-SEP-1999; 990S-0156596.
PR 04-OCT-1999; 990S-0157117.
PR 05-OCT-1999; 990S-0157753.
PR 06-OCT-1999; 990S-0157865.
PR 08-OCT-1999; 990S-0158029.
PR 12-OCT-1999; 990S-0158232.
PR 13-OCT-1999; 990S-0158369.
PR 13-OCT-1999; 990S-0159293.
PR 13-OCT-1999; 990S-0159294.
PR 14-OCT-1999; 990S-0159295.
PR 14-OCT-1999; 990S-0159329.
PR 14-OCT-1999; 990S-0159330.
PR 14-OCT-1999; 990S-0159331.
PR 14-OCT-1999; 990S-0159637.
PR 14-OCT-1999; 990S-0159638.
PR 18-OCT-1999; 990S-0159584.
PR 21-OCT-1999; 990S-0160741.
PR 21-OCT-1999; 990S-0160767.
PR 21-OCT-1999; 990S-0160768.
PR 21-OCT-1999; 990S-0160770.
PR 21-OCT-1999; 990S-0160814.
PR 21-OCT-1999; 990S-0160815.
PR 22-OCT-1999; 990S-0160980.
PR 22-OCT-1999; 990S-0160981.
PR 22-OCT-1999; 990S-0160989.
PR 25-OCT-1999; 990S-0161404.
PR 25-OCT-1999; 990S-0161405.
PR 25-OCT-1999; 990S-0161406.
PR 26-OCT-1999; 990S-0161359.
PR 26-OCT-1999; 990S-0161360.
PR 26-OCT-1999; 990S-0161361.
PR 28-OCT-1999; 990S-0161920.
PR 28-OCT-1999; 990S-0161922.
PR 28-OCT-1999; 990S-0161993.
PR 29-OCT-1999; 990S-0162142.

```

Query Match 11.4%; Score 250.8; DB 21; Length 1821;  
 Best Local Similarity 53.4%; Pred No. 1.6e-48;  
 Matches 675; Conservative 0; Mismatches 555; Indels 33; Gaps 6;

OY 631 tttagagctgaacctgaagcaacttgaaagagtgintgcggagccgatttcaatc 690  
 Db 550 tatcagagtgatcttgatgatctgaagaaagattgatgcgtcgagctgatctgtgt 609

```

OY 691 acgcagcttctcttgaagctgacacattctccgcttggaaagcgatgcacgacatg 750
Db 610 actcagcttctctatgatacgtatatactcccaagttctgaaatgattgcggcaatt 669
OY 751 ggcatacttgcgccatcgtcccggaattctccatcccgaggtcccaactccctcgg 810
Db 670 gggaattgctgccatgttcccggaattatgcctatatacttaactaactaagggcttttg 729
OY 811 cagcttctgaagctgtccaaagctggaagtgccaaagagatcaagacgttattgagca 870
Db 730 cgtatgactgttctctcgaagactaagatacacaagttagtgatgctgcgcttgaagcct 789
OY 871 atcaaaagacaagatgctgcacatccgaactatgctcgagctggccggtgagctgtgc 930
Db 790 atcaagatacagaagaagcgtgaaagccatagttatccactcttgaacagagatggt 849
OY 931 cagagctctcgcagatgctgtgtgccaagctcccaactctacaccccaacccgag 990
Db 850 aaaaagatgttgcgtcatgtgataagttc---ctcatctctacacattgaacatgag 906
OY 991 atggtctcaacagaagtgctggaagcgcctggagatgctggaactgagaccca---ggcgt 1047
Db 907 aaatctgtctcttgaatattgatatgttatgttatgtatgagttccaaaatttctcgt 966
OY 1048 cccctacccctgcgtctcagttgcccccacccaagcgcgagagagatgtaattcccatc 1107
Db 967 tctttaacccttgagaagcgcctctgcaaatgtttctccgtataagagaatgtgcgcccatc 1026
OY 1108 ttctgggctcgcagacaaagattacatcactacgtaaccaaagatgtgagcgatttccct 1167
Db 1027 ttctggaacaaacgctcaaaagactacattcttaagaccaaagcgctggagatttccca 1086
OY 1168 aagcgccgctggggcaattctcttccctgcgttgggagctgaaagactactacac 1227
Db 1087 caagcgcggtgggtgattatcagcagtgctcatatgtgactctcggtatctcagttc 1146
OY 1228 ttctacctgaagagaagtcctcccaagagagagctgtgagatgtggggagagcgctg 1287
Db 1147 tcaagctcgc-----cgagacgctgaaagaagaagcttcaaaagaatggtgtgccacgtg 1200
OY 1288 aacagtgaaagcaagtgctctngaaagttcttcttaacctctcgagagaacaaacgg 1347
Db 1201 aaaaagtgtgaagatactacagagaatcaagagagctcgtccttggaaaccttaaaagc 1260
OY 1348 aatgtgcacaaagtgccttgcctgccttggaacagatgagcccttgggggtgtgagccagc 1407
Db 1261 -----agtcctcgtctgaattagatgga-----ctcagcgcaagagatcgcgcgc 1302
OY 1408 ctgctgaagagagagctgtcgcggtgaaacgcgagagcatctccacatcaactcacag 1467
Db 1303 atataaagcagaactgataaagaatcaactccaagagcttcttgaccatcatagccaa 1362
OY 1468 cccaacataacgggaagcgcgtccctccgacccaactcgtgggtggtgccccagcgaggc 1527
Db 1363 ccatcagctcaacgcgagagatctgattccccaactgttgaatggggaggttctgttga 1422
OY 1528 tatgtcttcagaagcgcctacttaagatttctaacttcccgagagacagaggaagcact 1587
Db 1423 tatgtatacacaagcctatactagaagttcttctgcctcaaaaggaatataagctagctg 1482
OY 1588 ctgcaagtgctgaagaagtaacagagcgcggttcaattacacacttgcataatgaaaggt 1647
Db 1483 gtgagagaatgcaagctt---gcacatcgatatacttaactatgctgtgaaacaaagagaa 1539
OY 1648 gaaaacatcaccaatgcctccctgaactgcagcgaatgctgcaactgtgggaacttccct 1707
Db 1540 cagtggttatcgaacacttgcaccaagctgtagtgaatgcgttaacttggggagtttcccg 1599
OY 1708 gggcgagagatcatatcagacccacccgtagtggatcccgtaagcttgaatgtctggaaagac 1767
Db 1600 gctaaagaaatcatatcaacaaacactatcgatcccgtagcttcaacgctcggaagatc 1659
OY 1768 gaggccttgcctctgagattgagcgtgtgggaaagctgtatgagagagatcccgctcc 1827

```



PA (SEKH/) SEKHON J.

XX Rozen R, Sekhon J;

XX WPI; 2001-638509/73.

DR  
XX  
XX  
PT New antisense nucleic acids, which are methylenetetrahydrofolate  
PT reductase inhibitors, useful for treating, stabilizing or preventing  
PT cancer, e.g. breast carcinoma, colon carcinoma, colorectal carcinoma or  
PT neuroblastoma

PS Disclosure; Fig 12A: 68pp: English.

XX  
XX  
CC The invention relates to a non allele-specific antisense nucleic acids,  
CC which binds to methylenetetrahydrofolate reductase (MTHFR; EC 1.5.1.20)  
CC nucleic acids and inhibits MTHFR protein expression in a mammal. MTHFR  
CC catalyses the NADPH-linked reduction of 5,10-methylenetetrahydrofolate to  
CC 5-methylenetetrahydrofolate, a co-substrate for methylation of  
CC homocysteine to methionine. The invention provides potential therapy for  
CC individuals with MTHFR deficiency. The non allele-specific antisense  
CC nucleic acids are useful for treating, stabilizing or preventing cancer,  
CC particularly breast carcinoma, colon carcinoma, colorectal carcinoma,  
CC lung cancer, brain cancer, pancreatic cancer, kidney cell cancer,  
CC neuroblastoma, glioma and leukaemia. MTHFR cDNA probe is used in gene  
CC therapy. The present DNA sequence is human methylenetetrahydrofolate  
CC reductase (MTHFR) gene exon 2 with flanking intron sequences. Human MTHFR  
CC gene is mapped to chromosome 1p36.3.

SO Sequence 339 BP; 73 A; 108 C; 95 G; 63 T; 0 other;

Query Match 10.9%; Score 240.2; DB 22; Length 339;  
Best Local Similarity 98.8%; Pred. No. 2, 8e-46;

Matches 242; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 243 ctcaagtttgaccgagatgagcagagtggtgcccctacatagacgtgacctggcacc 302
DB 45 ctcaagtttgaccgagatgagcagagtggtgcccctacatagacgtgacctggcacc 104
QY 303 agcagtgaccctggctcagacaagaagacctctccatgatgatgcccagcaccgcgt 362
DB 105 agcagtgaccctggctcagacaagaagacctctccatgatgatgcccagcaccgcgt 164
QY 363 gaactactgtgacctgagagacacatcctgacatgacctgtgcgtcagcgcctgagaga 422
DB 165 gaactactgtgacctgagagacacatcctgacatgacctgtgcgtcagcgcctgagaga 224
QY 423 gatcacgggcatctgcacaagaactagacagctgggctgaggaacatcatggcgctcg 482
DB 225 gatcacgggcatctgcacaagaactagacagctgggctgaggaacatcatgtgcgctcg 284
QY 483 gggag 487
DB 285 gggag 289
```

Search completed: June 26, 2002, 17:35:07  
Job time: 7079 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 26, 2002, 15:32:23 ; Search time 82.36 Seconds  
(Without alignments)  
6549.431 Million cell updates/sec

Title: SEQ1MOD

Sequence: 2186  
1 aattcgcgagccatggtgaa.....acctagctactctgtctcta 2196

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/2/1na/5A.COMB.seq:\*  
2: /cgn2\_6/ptodata/2/1na/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/1na/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/1na/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/1na/PCROS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/1na/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2186.6	99.6	2219	3	US-08-738-000-3
2	2186.6	99.6	2219	4	US-09-258-928-3
3	2186.6	99.6	2220	4	US-08-738-000-1
4	2186.6	99.6	2220	4	US-09-258-928-1
5	2177.6	99.2	2187	4	US-09-318-448-1
6	119	5.4	120	4	US-09-218-114A-5
7	67.2	3.1	4848	4	US-08-955-957A-1
8	67.2	3.1	4848	4	US-08-955-957A-4
9	67.2	3.1	4848	4	US-08-955-957A-6
10	48.2	2.2	2187	4	US-09-318-448-1
11	48.2	2.2	2219	3	US-08-738-000-3
12	48.2	2.2	2219	4	US-09-258-928-3
13	48.2	2.2	2220	4	US-08-738-000-1
14	48.2	2.2	2220	4	US-09-258-928-1
15	48.2	2.2	7218	1	US-08-232-463-14
16	44.4	2.0	1449	4	US-08-858-207A-54
17	40.4	1.8	2155	2	US-08-095-728B-5
18	40.4	1.8	2155	5	PCT-US92-02320A-5
19	40.4	1.8	3036	1	US-08-306-691B-52
20	40.4	1.8	3036	2	US-08-095-728B-1
21	40.4	1.8	3036	5	PCT-US92-02320A-1
22	40.4	1.8	3511	3	US-08-892-747-13
23	38.4	1.7	1090	4	US-09-289-349-7
24	38.4	1.7	4858	3	US-08-436-332B-9
25	37.6	1.7	7218	1	US-08-232-463-14
26	37.6	1.7	7808	2	US-08-149-097D-22
27	37.2	1.7	7791	2	US-08-149-097D-23

28	37	1.7	510	4	US-09-516-914-8	Sequence 8, Appl1
29	37	1.7	14272	4	US-09-516-914-23	Sequence 23, Appl1
30	37	1.7	4411529	4	US-09-103-840A-1	Sequence 1, Appl1
31	36.8	1.7	2481	1	US-08-324-243-35	Sequence 35, Appl1
32	36.8	1.7	2481	1	US-08-532-390-35	Sequence 35, Appl1
33	36.8	1.7	2481	3	US-08-717-294-35	Sequence 35, Appl1
34	36.8	1.7	2481	5	PCT-US95-11511-35	Sequence 10, Appl1
35	36.8	1.7	3545	3	US-08-480-474-10	Sequence 10, Appl1
36	36.8	1.7	4808	2	US-08-231-193A-10	Sequence 10, Appl1
37	36.8	1.7	4808	2	US-08-486-273A-10	Sequence 10, Appl1
38	36.8	1.7	4808	3	US-08-940-086A-10	Sequence 10, Appl1
39	36.8	1.7	4808	4	US-08-940-035A-10	Sequence 10, Appl1
40	36.6	1.7	1147	2	US-08-761-277A-44	Sequence 10, Appl1
41	36.4	1.7	309	4	US-09-221-298-4	Sequence 44, Appl1
42	36.4	1.7	23673	4	US-09-773-816-1	Sequence 4, Appl1
43	36.2	1.6	624	2	US-08-381-881-3	Sequence 1, Appl1
44	36.2	1.6	624	4	US-09-281-221-3	Sequence 3, Appl1
45	36.2	1.6	1613	2	US-08-813-940-1	Sequence 1, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-738-000-3  
; Sequence 3, Application US/08738000  
; Patent No. 6074821  
; GENERAL INFORMATION:  
; TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETERAHYDROFOLATE  
; NUMBER OF INVENTION: REDUCTASE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: KLAUBER & JACKSON  
; STREET: Continental Plaza - 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/738,000  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/CA95/00314  
; FILING DATE: 25-MAY-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9410620.0  
; FILING DATE: 26-MAY-1994  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2219 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 13..1983  
; US-08-738-000-3

Query Match 99.6%; Score 2186.6; DB 3; Length 2219;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
0y 1 aattcgcgagccatggtgaaagcagcaggaacacagcagcctcaaccctgtgtgag 60

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 26, 2002, 15:41:08 ; Search time 3727.78 Seconds  
(Without alignments) 12744.915 Million cell updates/sec

Title: SEQIMOD  
Sequence: 2196  
1 aatccgagagccatggtgaa.....acctagctctctgtctcta 2196

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_NA\_Main:\*

```

1: /cgn2_6/ptodata/2/pna/US086_COMB.seq.*
2: /cgn2_6/ptodata/2/pna/US06_COMB.seq.*
3: /cgn2_6/ptodata/2/pna/US07_COMB.seq.*
4: /cgn2_6/ptodata/2/pna/US080_COMB.seq.*
5: /cgn2_6/ptodata/2/pna/US081_COMB.seq.*
6: /cgn2_6/ptodata/2/pna/US082_COMB.seq.*
7: /cgn2_6/ptodata/2/pna/US083_COMB.seq.*
8: /cgn2_6/ptodata/2/pna/US084_COMB.seq.*
9: /cgn2_6/ptodata/2/pna/US085_COMB.seq.*
10: /cgn2_6/ptodata/2/pna/US086_COMB.seq.*
11: /cgn2_6/ptodata/2/pna/US087_COMB.seq.*
12: /cgn2_6/ptodata/2/pna/US088_COMB.seq.*
13: /cgn2_6/ptodata/2/pna/US089_COMB.seq.*
14: /cgn2_6/ptodata/2/pna/US090_COMB.seq.*
15: /cgn2_6/ptodata/2/pna/US091_COMB.seq.*
16: /cgn2_6/ptodata/2/pna/US092_COMB.seq.*
17: /cgn2_6/ptodata/2/pna/US093_COMB.seq.*
18: /cgn2_6/ptodata/2/pna/US094_COMB.seq.*
19: /cgn2_6/ptodata/2/pna/US095A_COMB.seq.*
20: /cgn2_6/ptodata/2/pna/US095B_COMB.seq.*
21: /cgn2_6/ptodata/2/pna/US095C_COMB.seq.*
22: /cgn2_6/ptodata/2/pna/US095D_COMB.seq.*
23: /cgn2_6/ptodata/2/pna/US096A_COMB.seq.*
24: /cgn2_6/ptodata/2/pna/US096B_COMB.seq.*
25: /cgn2_6/ptodata/2/pna/US096C_COMB.seq.*
26: /cgn2_6/ptodata/2/pna/US096D_COMB.seq.*
27: /cgn2_6/ptodata/2/pna/US096E_COMB.seq.*
28: /cgn2_6/ptodata/2/pna/US097A_COMB.seq.*
29: /cgn2_6/ptodata/2/pna/US097C_COMB.seq.*
30: /cgn2_6/ptodata/2/pna/US097C_COMB.seq.*
31: /cgn2_6/ptodata/2/pna/US098A_COMB.seq.*
32: /cgn2_6/ptodata/2/pna/US098B_COMB.seq.*
33: /cgn2_6/ptodata/2/pna/US098C_COMB.seq.*
34: /cgn2_6/ptodata/2/pna/US099A_COMB.seq.*
35: /cgn2_6/ptodata/2/pna/US099B_COMB.seq.*
36: /cgn2_6/ptodata/2/pna/US099C_COMB.seq.*
37: /cgn2_6/ptodata/2/pna/US100_COMB.seq.*
38: /cgn2_6/ptodata/2/pna/US101_COMB.seq.*
39: /cgn2_6/ptodata/2/pna/US6000_COMB.seq.*
40: /cgn2_6/ptodata/2/pna/US6001_COMB.seq.*
41: /cgn2_6/ptodata/2/pna/US6002_COMB.seq.*
42: /cgn2_6/ptodata/2/pna/US6003_COMB.seq.*
43: /cgn2_6/ptodata/2/pna/US6004_COMB.seq.*

```

```

44: /cgn2_6/ptodata/2/pna/US6005_COMB.seq.*
45: /cgn2_6/ptodata/2/pna/US6006_COMB.seq.*
46: /cgn2_6/ptodata/2/pna/US6007_COMB.seq.*
47: /cgn2_6/ptodata/2/pna/US6008_COMB.seq.*
48: /cgn2_6/ptodata/2/pna/US6009_COMB.seq.*
49: /cgn2_6/ptodata/2/pna/US6010_COMB.seq.*
50: /cgn2_6/ptodata/2/pna/US6011_COMB.seq.*
51: /cgn2_6/ptodata/2/pna/US6012_COMB.seq.*
52: /cgn2_6/ptodata/2/pna/US6013_COMB.seq.*
53: /cgn2_6/ptodata/2/pna/US6015_COMB.seq.*
54: /cgn2_6/ptodata/2/pna/US6016_COMB.seq.*
55: /cgn2_6/ptodata/2/pna/US6017_COMB.seq.*
56: /cgn2_6/ptodata/2/pna/US6018_COMB.seq.*
57: /cgn2_6/ptodata/2/pna/US6019_COMB.seq.*
58: /cgn2_6/ptodata/2/pna/US6020_COMB.seq.*
59: /cgn2_6/ptodata/2/pna/US6021_COMB.seq.*
60: /cgn2_6/ptodata/2/pna/US6022_COMB.seq.*
61: /cgn2_6/ptodata/2/pna/US6023_COMB.seq.*
62: /cgn2_6/ptodata/2/pna/US6024_COMB.seq.*
63: /cgn2_6/ptodata/2/pna/US6025_COMB.seq.*
64: /cgn2_6/ptodata/2/pna/US6026_COMB.seq.*
65: /cgn2_6/ptodata/2/pna/US6027_COMB.seq.*
66: /cgn2_6/ptodata/2/pna/US6028_COMB.seq.*
67: /cgn2_6/ptodata/2/pna/US6029_COMB.seq.*
68: /cgn2_6/ptodata/2/pna/US6030_COMB.seq.*
69: /cgn2_6/ptodata/2/pna/US6031_COMB.seq.*
70: /cgn2_6/ptodata/2/pna/US6032_COMB.seq.*
71: /cgn2_6/ptodata/2/pna/US6033_COMB.seq.*
72: /cgn2_6/ptodata/2/pna/US6034_COMB.seq.*
73: /cgn2_6/ptodata/2/pna/US6035_COMB.seq.*
74: /cgn2_6/ptodata/2/pna/US6036_COMB.seq.*
75: /cgn2_6/ptodata/2/pna/US6036_COMB.seq.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2188	99.6	2196	25 US-09-658-655-15	Sequence 15, Appl
2	2188	99.6	2196	36 US-09-962-665-15	Sequence 15, Appl
3	2188	99.6	2196	36 US-09-962-677-15	Sequence 15, Appl
4	2188	99.6	2196	31 US-09-963-333-15	Sequence 15, Appl
5	2186.6	99.6	2196	31 US-09-802-640-33	Sequence 33, Appl
6	2186.6	99.6	2219	22 US-09-592-595-3	Sequence 3, Appl1
7	2186.6	99.6	2219	26 US-09-660-872-3	Sequence 3, Appl1
8	2186.6	99.6	2219	26 US-09-660-872A-3	Sequence 3, Appl1
9	2186.6	99.6	2219	26 US-09-660-872A-3	Sequence 3, Appl1
10	2186.6	99.6	2219	26 US-09-660-872A-3	Sequence 3, Appl1
11	2186.6	99.6	2220	22 US-09-592-595A-1	Sequence 1, Appl1
12	2186.6	99.6	2220	26 US-09-660-872A-1	Sequence 1, Appl1
13	2186.6	99.6	2220	26 US-09-660-872A-1	Sequence 1, Appl1
14	2186.6	99.6	2220	26 US-09-660-872A-1	Sequence 1, Appl1
15	2186.6	99.6	2220	26 US-09-660-872A-1	Sequence 1, Appl1
16	2177.6	99.2	2187	17 US-09-371-347-51	Sequence 1, Appl1
17	2177.6	99.2	2187	17 US-09-371-347-51	Sequence 1, Appl1
18	2173.8	99.0	3485	66 US-60-278-258-99	Sequence 51, Appl1
19	2173.8	99.0	5979	71 US-60-324-185-1968	Sequence 99, Appl1
20	2172.2	98.9	2340	18 US-09-471-275-2157	Sequence 168, Ap
21	1961.6	89.3	1971	17 PCT-US01-26488-2	Sequence 2157, Ap
22	1961.6	89.3	1971	17 US-09-347-878-23	Sequence 2, Appl1
23	1961.6	89.3	1971	18 US-09-457-205-23	Sequence 23, Appl1
24	1961.6	89.3	1971	18 US-09-457-205-23	Sequence 23, Appl1
25	606	26.8	1465	75 US-60-360-207-6463	Sequence 6463, Ap
26	588.2	26.8	707	64 US-09-758-471-1373	Sequence 1373, Ap
27	469.4	21.4	569	64 US-60-252-833-25106	Sequence 1403, A
28	434.4	19.8	23748	1 PCT-US01-01339-2764	Sequence 2764, Ap
29	434.4	19.8	23748	1 PCT-US01-01339-2764	Sequence 2764, Ap
30	434.4	19.8	23748	30 US-09-764-891-7917	Sequence 7917, Ap
31	434.4	19.8	23748	37 US-10-080-090-2764	Sequence 2764, Ap

```
32 434.4 19.8 32768 60 US-60-213-177-379 Sequence 379, App
33 433.2 19.7 18542 1 PCT-US01-26488-1 Sequence 1, Appl
34 433.4 17.9 489 16 US-09-277-227-19340 Sequence 19340, A
35 433.4 17.9 489 17 US-09-346-956-16939 Sequence 16939, A
36 433.4 17.9 489 34 US-09-904-703-16939 Sequence 16939, A
37 433.4 17.9 489 34 US-09-909-627-19340 Sequence 19340, A
38 433.2 17.9 399 17 US-09-362-510-58537 Sequence 58537, A
39 433.2 17.9 399 17 US-09-362-510-58537 Sequence 58537, A
40 433.2 17.9 399 34 US-09-904-013-58537 Sequence 58537, A
C 41 387.2 17.6 400 18 US-09-489-036-12440 Sequence 12440, Ap
C 42 387.2 17.6 400 35 US-09-943-143-12440 Sequence 12440, Ap
43 373.8 17.0 378 19 US-09-528-409-52118 Sequence 52118, A
44 373.8 17.0 378 35 US-09-933-524-52118 Sequence 52118, A
45 373.8 17.0 378 35 US-09-933-524A-52118 Sequence 52118, A
```

## ALIGNMENTS

```
RESULT 1
US-09-658-659-15
; Sequence 15 Application US/09658659
; GENERAL INFORMATION:
; APPLICANT: Stanlon, Jr., Vincent P.
; TITLE OF INVENTION: GENE SEQUENCE VARIANCE IN GENES RELATED
; TITLE OF INVENTION: TO FOLATE METABOLISM HAVING UTILITY IN DETERMINING THE
; FILE REFERENCE: 11926-015001
; CURRENT APPLICATION NUMBER: US/09/658,659
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/596,033
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 09/357,743
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/357,024
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: 60/093,484
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: misc_feature
; LOCATION: 1784
; OTHER INFORMATION: n = a or g
; NAME/KEY: misc_feature
; LOCATION: 464
; OTHER INFORMATION: n = g or t
; NAME/KEY: misc_feature
; LOCATION: 120, 519, 668, 1059, 1308
; OTHER INFORMATION: n = c or t
; NAME/KEY: misc_feature
; LOCATION: 1289
; OTHER INFORMATION: n = c or a
US-09-658-659-15

Query Match          99.6%; Score 2188; DB 25; Length 2196;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2191; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 aattccgagcagtgatgaagcagaggaacacagcctcaacccctgttgag 60
Db 1 aattccgagcagtgatgaagcagaggaacacagcctcaacccctgttgag 60
QY 61 ggcagtgacagcagtgatgaagcagaggaacacagcctcaacccctgttgag 120
Db 61 ggcagtgacagcagtgatgaagcagaggaacacagcctcaacccctgttgag 120
```

```
QY 121 ctgaccctgagcgcagtgagagacatccggagagagatgaagcgcgcatgtgaatctg 180
Db 121 ctgaccctgagcgcagtgagagacatccggagagagatgaagcgcgcatgtgaatctg 180
QY 181 gacaagtgtctctccctgaatcttccctccctccctgaactgtgagagagctgacatctc 240
Db 181 gacaagtgtctctccctgaatcttccctccctccctgaactgtgagagagctgacatctc 240
QY 241 atcccaagtgatcccgagatgagcagagtggtccctccatagaagcgtgactggcac 300
Db 241 atcccaagtgatcccgagatgagcagagtggtccctccatagaagcgtgactggcac 300
QY 301 ccagcagtgacccctgctcagacaaagagacatccctccatgatgacgcagcacgcgc 360
Db 301 ccagcagtgacccctgctcagacaaagagacatccctccatgatgacgcagcacgcgc 360
QY 361 gtgaactactgtgctcgtgagacatctctcagatgacatgctgcgtgcgcgcgcgcgcgc 420
Db 361 gtgaactactgtgctcgtgagacatctctcagatgacatgacatgctgcgtgcgcgcgcgcgc 420
QY 421 gagatcacggccatctgacacaaagctaaagcagctggcctgaggaacatcatgagcgcgc 480
Db 421 gagatcacggccatctgacacaaagctaaagcagctggcctgaggaacatcatgagcgcgcgc 480
QY 481 cggggagacccaatagtgaccagtgaggagagagagagagagagagagagagagagagagag 540
Db 481 cggggagacccaatagtgaccagtgaggagagagagagagagagagagagagagagagagagag 540
QY 541 gacctgtgagacacatccgaagtgatgttgagacttgaacttgaacttgaacttgaacttga 600
Db 541 gacctgtgagacacatccgaagtgatgttgagacttgaacttgaacttgaacttgaacttga 600
QY 541 gacctgtgagacacatccgaagtgatgttgagacttgaacttgaacttgaacttgaacttga 600
Db 541 gacctgtgagacacatccgaagtgatgttgagacttgaacttgaacttgaacttgaacttga 600
QY 601 taccccaagagccaccccgagagagagagagagagagagagagagagagagagagagagag 660
Db 601 taccccaagagccaccccgagagagagagagagagagagagagagagagagagagagagag 660
QY 661 aaggtgtgacggagacgattcatcatcagcagcttcttgaagctgaagctgaagctgaagctga 720
Db 661 aaggtgtgacggagacgattcatcatcagcagcttcttgaagctgaagctgaagctgaagctga 720
QY 721 ttcgccttctgagagcagtcagcagacatgagcagcagcagcagcagcagcagcagcagcagc 780
Db 721 ttcgccttctgagagcagtcagcagacatgagcagcagcagcagcagcagcagcagcagcagc 780
QY 781 tttcccatcagagcagtcacatccctctgagcagctgtgaagctgtgcaagctgtgagagtg 840
Db 781 tttcccatcagagcagtcacatccctctgagcagctgtgaagctgtgcaagctgtgagagtg 840
QY 841 ccacagagatcaagagcagtgatgagcagcagcagcagcagcagcagcagcagcagcagcagc 900
Db 841 ccacagagatcaagagcagtgatgagcagcagcagcagcagcagcagcagcagcagcagcagc 900
QY 901 tatgcatgagcagtcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 960
Db 901 tatgcatgagcagtcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 960
QY 961 ggcctccatcttcaacccctcaaccccgagatgagctgacacacagagagagagagagagagag 1020
Db 961 ggcctccatcttcaacccctcaaccccgagatgagctgacacacagagagagagagagagagag 1020
QY 1021 gggatgtgagcagtgagaccccgagcgtccctcactacccctgagcagcagcagcagcagc 1080
Db 1021 gggatgtgagcagtgagaccccgagcgtccctcactacccctgagcagcagcagcagcagc 1080
QY 1081 cgcgagagagagagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1140
Db 1081 cgcgagagagagagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1140
QY 1141 cgtacccagagagagagagagagagagagagagagagagagagagagagagagagagagagagag 1200
Db 1141 cgtacccagagagagagagagagagagagagagagagagagagagagagagagagagagagagag 1200
QY 1201 ttgggagagcagagagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1260
```



```

Db 1201 ttctgggggagcgaagactactactctctcctcgaagagcaagctccccaagagagag 1260
Qy 1261 ctgctgaagatgtggtgggagagctgancagtgaaagtgatctctgaaagcttctgtt 1320
Db 1261 ctgctgaagatgtggtgggagagctgancagtgaaagtgatctctgaaagcttctgtt 1320
Qy 1321 cttaacctctggtgagaaaccaaacggaatggtacaaagtgaacttgctctccctgagac 1380
Db 1321 cttaacctctggtgagaaaccaaacggaatggtacaaagtgaacttgctctccctgagac 1380
Qy 1381 gatgagccctctggtgagaaaccaacctgctgtaagagagagagctgctgagagagagac 1440
Db 1381 gatgagccctctggtgagaaaccaacctgctgtaagagagagagctgctgagagagac 1440
Qy 1441 caggagcactctcaccatcaccatcaccagcccaacaaacggaagagagagagagagagac 1500
Db 1441 caggagcactctcaccatcaccatcaccagcccaacaaacggaagagagagagagagac 1500
Qy 1501 atcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1560
Db 1501 atcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1560
Qy 1561 actcccgagagagagagagagagagagagagagagagagagagagagagagagagagag 1620
Db 1561 actcccgagagagagagagagagagagagagagagagagagagagagagagagagagag 1620
Qy 1621 aattaccactctgcaatgtaagtgatgtaagtgatgtaagtgatgtaagtgatgtaagtgat 1680
Db 1621 aattaccactctgcaatgtaagtgatgtaagtgatgtaagtgatgtaagtgatgtaagtgat 1680
Qy 1681 aatgtgtcactctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1740
Db 1681 aatgtgtcactctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1740
Qy 1741 cccgtcagctcactggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1800
Db 1741 cccgtcagctcactggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1800
Qy 1801 aagctgtatgagagagagagagagagagagagagagagagagagagagagagagagagag 1860
Db 1801 aagctgtatgagagagagagagagagagagagagagagagagagagagagagagagagag 1860
Qy 1861 ttctgtgttaactggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1920
Db 1861 ttctgtgttaactggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1920
Qy 1921 gaagacacatgtgagagagagagagagagagagagagagagagagagagagagagagagag 1980
Db 1921 gaagacacatgtgagagagagagagagagagagagagagagagagagagagagagagagag 1980
Qy 1981 tgaacctgctgctgagagagagagagagagagagagagagagagagagagagagagagagag 2040
Db 1981 tgaacctgctgctgagagagagagagagagagagagagagagagagagagagagagagagag 2040
Qy 2041 ggtgctgctctctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 2100
Db 2041 ggtgctgctctctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 2100
Qy 2101 ccccaactgacaaatgagagagagagagagagagagagagagagagagagagagagagagagag 2160
Db 2101 ccccaactgacaaatgagagagagagagagagagagagagagagagagagagagagagagagag 2160
Qy 2161 tgggccccacatggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 2196
Db 2161 tgggccccacatggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 2196

```

```

RESULT 2
US-09-962-665-15
: Sequence 15, Application US/09962665
: GENERAL INFORMATION:
: APPLICANT: Stanton, Jr., Vincent P.

```

```

: TITLE OF INVENTION: POLY(POLYGLUTAMATE SYNTHETASE GENE SEQUENCE
: TITLE OF INVENTION: VARIANCES HAVING UTILITY IN DETERMINING THE
: FILE REFERENCE: 11926-015004
: CURRENT APPLICATION NUMBER: US/09/962,665
: CURRENT FILING DATE: 2001-09-24
: PRIOR APPLICATION NUMBER: 09/658,659
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 09/596,033
: PRIOR FILING DATE: 2000-06-15
: PRIOR APPLICATION NUMBER: 09/357,743
: PRIOR FILING DATE: 1999-07-20
: PRIOR APPLICATION NUMBER: 09/357,024
: PRIOR FILING DATE: 1999-07-19
: PRIOR APPLICATION NUMBER: 60/093,484
: PRIOR FILING DATE: 1998-07-20
: NUMBER OF SEQ. ID NOS: 16
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ. ID NO 15
: LENGTH: 2196
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic construct
: NAME/KEY: misc_feature
: LOCATION: 1784
: OTHER INFORMATION: n = a or g
: NAME/KEY: misc_feature
: LOCATION: 464
: OTHER INFORMATION: n = g or t
: NAME/KEY: misc_feature
: LOCATION: 120, 519, 668, 1059, 1308
: OTHER INFORMATION: n = c or t
: NAME/KEY: misc_feature
: LOCATION: 1289
: OTHER INFORMATION: n = c or a
US-09-962-665-15

```

```

Query Match 99.6%; Score 2188; DB 36; Length 2196;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2191; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 aattccggagcagctgtgagagagagagagagagagagagagagagagagagagagagagag 60
Db 1 aattccggagcagctgtgagagagagagagagagagagagagagagagagagagagagagag 60
Qy 61 ggcagtgccagcagctgtgagagagagagagagagagagagagagagagagagagagagagag 120
Db 61 ggcagtgccagcagctgtgagagagagagagagagagagagagagagagagagagagagagag 120
Qy 121 ctggaacctgagcagctgtgagagagagagagagagagagagagagagagagagagagagag 180
Db 121 ctggaacctgagcagctgtgagagagagagagagagagagagagagagagagagagagagag 180
Qy 181 gacaagtgttccctggaattcttccctcctggaactgctggaactgctggaactgctggaact 240
Db 181 gacaagtgttccctggaattcttccctcctggaactgctggaactgctggaactgctggaact 240
Qy 241 atctcaaggttctcctctggaattcttccctcctggaactgctggaactgctggaactgctgga 300
Db 241 atctcaaggttctcctctggaattcttccctcctggaactgctggaactgctggaactgctgga 300
Qy 301 cgaagaggttgacacctggtctgagacaaagagagagagagagagagagagagagagagagagag 360
Db 301 cgaagaggttgacacctggtctgagacaaagagagagagagagagagagagagagagagagagag 360
Qy 361 gtaactactgtgctgtgagagagagagagagagagagagagagagagagagagagagagagag 420
Db 361 gtaactactgtgctgtgagagagagagagagagagagagagagagagagagagagagagagag 420
Qy 421 gagatcacgggacatctgacacaaagctaaagagctgggcttgaggaacatctgagcgtg 480

```

Db 421 gaatacagggccatctgcaacaaagcagctgagcctganaacatcatgagctg 480  
QY 481 cgggaggaacccaataggtgaccagtggaagaggaagagagcttcaactacgacgtg 540  
Db 481 cgggaggaacccaataggtgaccagtggaagaggaagagagcttcaactacgacgtg 540  
QY 541 gacctgtggaagacacatccgaagtgagcttctgtgactactcttgaacatcggtgacagt 600  
Db 541 gacctgtggaagacacatccgaagtgagcttctgtgactactcttgaacatcggtgacagt 600  
QY 601 taacccaagaagccaccgcaagcagagccttgaagctgacatcgtgaagcactggaagag 660  
Db 601 taacccaagaagccaccgcaagcagagccttgaagctgacatcgtgaagcactggaagag 660  
QY 661 aaggtgtgagcagagccgacttcatcatcagcagccttcttgaagctgacacatc 720  
Db 661 aaggtgtgagcagagccgacttcatcatcagcagccttcttgaagctgacacatc 720  
QY 721 ttccgcttctggaagcagcagccacatgagcacttgcacacatcgtcccgagac 780  
Db 721 ttccgcttctggaagcagcagccacatgagcacttgcacacatcgtcccgagac 780  
QY 781 ttccccaacagagctacacatccctctcgagcagctgtgaagctgtccaaagctgagagtg 840  
Db 781 ttccccaacagagctacacatccctctcgagcagctgtgaagctgtccaaagctgagagtg 840  
QY 841 ccaacagagatcaagagcgtgattgagcacaatcaagacacagatctgcatccgcaac 900  
Db 841 ccaacagagatcaagagcgtgattgagcacaatcaagacacagatctgcatccgcaac 900  
QY 901 tatgtgacatcgagctgagcagtgagcagtgagcagagcttctgagcagtggtgtgacaa 960  
Db 901 tatgtgacatcgagctgagcagtgagcagtgagcagagcttctgagcagtggtgtgacaa 960  
QY 961 ggcctccacttcaacacccctcaacgagagatgagctgacacacagagtggtgaaagcgctg 1020  
Db 961 ggcctccacttcaacacccctcaacgagagatgagctgacacacagagtggtgaaagcgctg 1020  
QY 1021 gggatgtgagctgagagaccccaagcagctccctacacctgagctcagtgctccaccccaag 1080  
Db 1021 gggatgtgagctgagagaccccaagcagctccctacacctgagctcagtgctccaccccaag 1080  
QY 1081 cgcagagagagagatgtaagctccatctctgagccttccagacacaaagtgtaactac 1140  
Db 1081 cgcagagagagagatgtaagctccatctctgagccttccagacacaaagtgtaactac 1140  
QY 1141 cgtaccagaagctgagagcagatctccctaaacgagcagctgagagcaattccctccctgac 1200  
Db 1141 cgtaccagaagctgagagcagatctccctaaacgagcagctgagagcaattccctccctgac 1200  
QY 1201 ttgagagagctgagagagactactactcttcttactgagagagcaagtcacccaagagag 1260  
Db 1201 ttgagagagctgagagagactactactcttcttactgagagagcaagtcacccaagagag 1260  
QY 1261 ctgctgaagagctgagagagagctgagcagtgagcagagagtgcttgaagcttctt 1320  
Db 1261 ctgctgaagagctgagagagagctgagcagtgagcagagagtgcttgaagcttctt 1320  
QY 1321 ctttaacctctggagagacacaaacggaatggttcaacaaagtgaactgtgctgacctgagac 1380  
Db 1321 ctttaacctctggagagacacaaacggaatggttcaacaaagtgaactgtgctgacctgagac 1380  
QY 1381 gatgagccctggagcagctgagacacagcctgttgaagagagagagctgctgagtgagac 1440  
Db 1381 gatgagccctggagcagctgagacacagcctgttgaagagagagagctgctgagtgagac 1440  
QY 1441 cagggacatccatcaatcaatcaacagcccaacatcaacaggaagcgttccctcgacccc 1500  
Db 1441 cagggacatccatcaatcaatcaacagcccaacatcaacaggaagcgttccctcgacccc 1500  
QY 1501 atcgtgagctgagcagccagaggggagctatgtcttccagagagcctactagagtttcc 1560  
Db 1501 atcgtgagctgagcagccagaggggagctatgtcttccagagagcctactagagtttcc 1560

QY 1561 acttcccgagagacagcgggaagcacttctgcaagtgtctgaagaagtacagctccggtt 1620  
Db 1561 acttcccgagagacagcgggaagcacttctgcaagtgtctgaagaagtacagctccggtt 1620  
QY 1621 aattaccacactgttcaagtgtgaaggtgnaaaacatcaacccaatgcccctgaactgacagccg 1680  
Db 1621 aattaccacactgttcaagtgtgaaggtgnaaaacatcaacccaatgcccctgaactgacagccg 1680  
QY 1681 aatgtgtcaacttggggagcattctccctggcgagagatcatccagccacgtaagtgt 1740  
Db 1681 aatgtgtcaacttggggagcattctccctggcgagagatcatccagccacgtaagtgt 1740  
QY 1741 cccgtcaagcttcaatgttctggaagagcagagcgttctgcccctgtagattgagcgtgagga 1800  
Db 1741 cccgtcaagcttcaatgttctggaagagcagagcgttctgcccctgtagattgagcgtgagga 1800  
QY 1801 aagctgtatgagagagaggtcccccgtcccgcaacatcatcatcagtatcatccagacaattac 1860  
Db 1801 aagctgtatgagagagaggtcccccgtcccgcaacatcatcatcagtatcatccagacaattac 1860  
QY 1861 ttctgtgtcaacctgtgtggaacatagacttcccaactggaacactgctctgtgaggtgtg 1920  
Db 1861 ttctgtgtcaacctgtgtggaacatagacttcccaactggaacactgctctgtgaggtgtg 1920  
QY 1921 gaagacacatgtgagcttctcaacagagccaccccaagaaatgagagaaacgagagctcca 1980  
Db 1921 gaagacacatgtgagcttctcaacagagccaccccaagaaatgagagaaacgagagctcca 1980  
QY 1981 tgacctgtctccttgaagcagcagctgtgagagcacttctgctccgcttccctccacaca 2040  
Db 1981 tgacctgtctccttgaagcagcagctgtgagagcacttctgctccgcttccctccacaca 2040  
QY 2041 gtgtgtcttctcttgggaactcactctcctctgtgtcttccaccccgagctcactac 2100  
Db 2041 gtgtgtcttctcttgggaactcactctcctctgtgtcttccaccccgagctcactac 2100  
QY 2101 ccccaactgacaaatgagcagctgagctgagtgagagcttccagagccttcccgagcgtgag 2160  
Db 2101 ccccaactgacaaatgagcagctgagctgagtgagagcttccagagccttcccgagcgtgag 2160  
QY 2161 tcggcccaacatggaacctagtaactctctgctcta 2196  
Db 2161 tcggcccaacatggaacctagtaactctctgctcta 2196

RESULT 3  
US-09-962-677-15  
Sequence 15, Application US/09962677  
GENERAL INFORMATION:  
APPLICANT: Stanton, Jr., Vincent P.  
TITLE OF INVENTION: THYMIDINE PHOSPHORYLASE GENE SEQUENCE  
TITLE OF INVENTION: VARIANCES HAVING UTILITY IN DETERMINING  
FILE REFERENCE: 11926-015003  
CURRENT FILING DATE: 2001-09-24  
PRIOR APPLICATION NUMBER: 09/658,659  
PRIOR FILING DATE: 2000-09-08  
PRIOR APPLICATION NUMBER: 09/596,033  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 09/357,743  
PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 09/357,024  
PRIOR FILING DATE: 1999-07-19  
PRIOR APPLICATION NUMBER: 60/093,484  
PRIOR FILING DATE: 1998-07-20  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 2196  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
: OTHER INFORMATION: Synthetic construct  
: NAME/KEY: misc\_feature  
: LOCATION: 1784  
: OTHER INFORMATION: n = a or g  
: NAME/KEY: misc\_feature  
: LOCATION: 464  
: OTHER INFORMATION: n = g or t  
: NAME/KEY: misc\_feature  
: LOCATION: 120, 519, 668, 1059, 1308  
: OTHER INFORMATION: n = c or t  
: NAME/KEY: misc\_feature  
: LOCATION: 1289  
: OTHER INFORMATION: n = c or a  
US-09-962-677-15

Query Match 99.6%; Score 2188; DB 36; Length 2196;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2191; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 aatccgagccatggtggaagcgaagcaaacgcaacccccaacccctgttgag 60  
Db 1 aatccgagccatggtggaagcgaagcaaacgcaacccccaacccctgttgag 60  
QY 61 ggcagtgccagcagtgagcagtgagcagtcaccaagatagttcgaagatgttccaccccgagc 120  
Db 61 ggcagtgccagcagtgagcagtgagcagtcaccaagatagttcgaagatgttccaccccgagc 120  
QY 121 ctgagaccctgagcgcatgagagaccccgagagagatgagcgagcttgagaaatctggt 180  
Db 121 ctgagaccctgagcgcatgagagaccccgagagagatgagcgagcttgagaaatctggt 180  
QY 181 gacaaagtgttctccctgggaattcttcctctctgaactgtctggggagagctgtcaatctc 240  
Db 181 gacaaagtgttctccctgggaattcttcctctctgaactgtctggggagagctgtcaatctc 240  
QY 241 atctcaaggtttgacccgagatgagcaggttgcccccctctacatagacgttgacttgagac 300  
Db 241 atctcaaggtttgacccgagatgagcaggttgcccccctctacatagacgttgacttgagac 300  
QY 301 ccagcaggtgacccctgtgctcagagacagagacccctccatgatgatctgcgcagacccgc 360  
Db 301 ccagcaggtgacccctgtgctcagagacagagacccctccatgatgatctgcgcagacccgc 360  
QY 361 gtaactactgtgctcgtgagacacatctctgacatgacctgcgtgcgtcagcgcttgag 420  
Db 361 gtaactactgtgctcgtgagacacatctctgacatgacctgcgtgcgtcagcgcttgag 420  
QY 421 gagaatcagcgccatctgacacaaagttaagcagcttgagcctgaggaacatcatgtgcgtg 480  
Db 421 gagaatcagcgccatctgacacaaagttaagcagcttgagcctgaggaacatcatgtgcgtg 480  
QY 481 cggggagaccccaatagtgagcagtgaggagagagagagagagagagagagagagagagag 540  
Db 481 cggggagaccccaatagtgagcagtgaggagagagagagagagagagagagagagagagag 540  
QY 541 gacctgtgagacacatcccaagtgagttcgtgactacttgacatctgtgtgagagat 600  
Db 541 gacctgtgagacacatcccaagtgagttcgtgactacttgacatctgtgtgagagat 600  
QY 601 taccccaaaagccaccgcagagcaggttgaggttgagccttgacacgtgaagcacttgaagag 660  
Db 601 taccccaaaagccaccgcagagcaggttgaggttgagccttgacacgtgaagcacttgaagag 660  
QY 661 aaggtgtgtgagcagcagattcatcatcagcagatttcttgagggtgtgacatctc 720  
Db 661 aaggtgtgtgagcagcagattcatcatcagcagatttcttgagggtgtgacatctc 720  
QY 721 ttccgcttgtgagagcagtcacagacatgagcatcacttgcccatcgctcccgagatc 780  
Db 721 ttccgcttgtgagagcagtcacagacatgagcatcacttgcccatcgctcccgagatc 780

QY 781 ttcccatccagagcgtacacactcccttcggcagcttgtagaagctgtccaaagctgagagt 840  
Db 781 ttcccatccagagcgtacacactcccttcggcagcttgtagaagctgtccaaagctgagagt 840  
QY 841 ccacagagatcaaaagagctgtagtgagccaatcaaaagacaaagatgtgcatcccgcaac 900  
Db 841 ccacagagatcaaaagagctgtagtgagccaatcaaaagacaaagatgtgcatcccgcaac 900  
QY 901 tatgcatcagagctgctgcgtgagcctgtgacagagactctgagcaagtgtgctgtgcca 960  
Db 901 tatgcatcagagctgctgcgtgagcctgtgacagagactctgagcaagtgtgctgtgcca 960  
QY 961 ggcctccacttccacacccctcaaccccgagagatggtctacacagaggtgtcgaagcctg 1020  
Db 961 ggcctccacttccacacccctcaaccccgagagatggtctacacagaggtgtcgaagcctg 1020  
QY 1021 gggatgtgagctgagagacccacagcgctccctacacttcgctctacgtgcccaccccaag 1080  
Db 1021 gggatgtgagctgagagacccacagcgctccctacacttcgctctacgtgcccaccccaag 1080  
QY 1081 cgcgagagagagatgtacgtcccatctctgagcctccacagacaaagatlaacatcac 1140  
Db 1081 cgcgagagagagatgtacgtcccatctctgagcctccacagacaaagatlaacatcac 1140  
QY 1141 cgtaccacagaggttgagcagattccctacagcgcgcttgagggaattctctctccctgccc 1200  
Db 1141 cgtaccacagaggttgagcagattccctacagcgcgcttgagggaattctctctccctgccc 1200  
QY 1201 ttggggagcctgaaagagatactacactctctacactgaaagagcaagctccccaagagagag 1260  
Db 1201 ttggggagcctgaaagagatactacactctctacactgaaagagcaagctccccaagagagag 1260  
QY 1261 ctgctgaaagatgttgaggagagagctgancagtgaaagcaagtgtcttngaagcttctgt 1320  
Db 1261 ctgctgaaagatgttgaggagagagctgancagtgaaagcaagtgtcttngaagcttctgt 1320  
QY 1321 cttaacctctggagaaacccaacccggaatgttcaacaaagagacttgcttccctggagac 1380  
Db 1321 cttaacctctggagaaacccaacccggaatgttcaacaaagagacttgcttccctggagac 1380  
QY 1381 gatgagccctctgagcgtgaaagacagcctgtgaaagagagagctgctcggtgaaacgc 1440  
Db 1381 gatgagccctctgagcgtgaaagacagcctgtgaaagagagagctgctcggtgaaacgc 1440  
QY 1441 caggagcattccctcaacatcaaatcaacagcccaacatcaacagggagagcgctctccgacccc 1500  
Db 1441 caggagcattccctcaacatcaaatcaacagcccaacatcaacagggagagcgctctccgacccc 1500  
QY 1501 atcgtgagctgagccccaagcggtgatagttcttccagaaagagcctacttagaatttctc 1560  
Db 1501 atcgtgagctgagccccaagcggtgatagttcttccagaaagagcctacttagaatttctc 1560  
QY 1561 acttcccgagagacagcggaagcactctctgcaagtgtcgaagagtaagagctccggtt 1620  
Db 1561 acttcccgagagacagcggaagcactctctgcaagtgtcgaagagtaagagctccggtt 1620  
QY 1621 aattaacaccttgcaatgtgaaggtgaaagaaatcaacccaatgacctgaaactgcaacgcg 1680  
Db 1621 aattaacaccttgcaatgtgaaggtgaaagaaatcaacccaatgacctgaaactgcaacgcg 1680  
QY 1681 aatgtctcaacttgaggacatcttccctggcgagagagatcatccagccacacgtgtgagat 1740  
Db 1681 aatgtctcaacttgaggacatcttccctggcgagagagatcatccagccacacgtgtgagat 1740  
QY 1741 ccggtcaagctcatgtctctggaagagcagagccttgcctctgtagatgtgagcgtgtggga 1800  
Db 1741 ccggtcaagctcatgtctctggaagagcagagccttgcctctgtagatgtgagcgtgtggga 1800  
QY 1801 aagctgtatgagagagagctcccgctccgacacataatcaagatacatccagacacataac 1860  
Db 1801 aagctgtatgagagagagctcccgctccgacacataatcaagatacatccagacacataac 1860  
QY 1861 ttctgtgtcaacctgtgtgacaatgacttccaatgacaacatgtcctctgagaggtgtg 1920

```
Db 1861 ttccctgtcaacctgtgtgaacaatgacttcccaactggaacaactgctctgtgaggtgtg 1920
Qy 1921 gaagacaatttgagcttctcaacagcccccacaagaatgagagaagaagaggtctcca 1980
Db 1921 gaagacaatttgagcttctcaacagcccccacaagaatgagagaagaagaggtctcca 1980
Qy 1981 tgacctgtctctgtgagccctgtgtgagagccactctgtccgcctctctctccaca 2040
Db 1981 tgacctgtctctgtgagccctgtgtgagagccactctgtccgcctctctctctccaca 2040
Qy 2041 gtgtgtctctctgtggaactcaactctctgtgtctctctccaccgcgctctcaactc 2100
Db 2041 gtgtgtctctctgtggaactcaactctctgtgtctctctccaccgcgctctcaactc 2100
Qy 2101 ccccaactgacaatgagcaactgagctggagtgaggttccagagctcttcttgagactgag 2160
Db 2101 ccccaactgacaatgagcaactgagctggagtgaggttccagagctcttcttgagactgag 2160
Qy 2161 tcggccccacatggaagcaactgagctctgtctcta 2196
Db 2161 tcggccccacatggaagcaactgagctctgtctcta 2196
```

```
RESULT 4
US-09-963-333-15
/ Sequence 15, Application US/09963333
/ GENERAL INFORMATION:
/ APPLICANT: Stanton, Jr., Vincent P.
/ TITLE OF INVENTION: THYMIDINE SYNTHASE GENE SEQUENCE VARIANCES
/ TITLE OF INVENTION: HAVING UTILITY IN DETERMINING THE TREATMENT
/ FILE OF INVENTION: OF DISEASE
/ FILE REFERENCE: 11926-015002
/ CURRENT FILING DATE: 2001-09-24
/ PRIOR APPLICATION NUMBER: US/09/963,333
/ PRIOR FILING DATE: 2000-09-08
/ PRIOR APPLICATION NUMBER: 09/596,033
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 09/357,743
/ PRIOR FILING DATE: 1999-07-20
/ PRIOR APPLICATION NUMBER: 09/357,024
/ PRIOR FILING DATE: 1999-07-19
/ PRIOR APPLICATION NUMBER: 60/093,484
/ PRIOR FILING DATE: 1998-07-20
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 15
/ LENGTH: 2196
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
/ NAME/KEY: misc_feature
/ LOCATION: 1784
/ OTHER INFORMATION: n = a or g
/ NAME/KEY: misc_feature
/ LOCATION: 464
/ OTHER INFORMATION: n = g or t
/ NAME/KEY: misc_feature
/ LOCATION: 120, 519, 668, 1059, 1308
/ OTHER INFORMATION: n = c or t
/ NAME/KEY: misc_feature
/ LOCATION: 1289
/ OTHER INFORMATION: n = c or a
/ US-09-963-333-15
```

```
Query Match 99.6%; Score 2188; DB 36; Length 2196;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2191; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy 1 aatccgagccatgtgtgaacgaagccagagaagaacagcagctcaacccctgtctgag 60
```

```
Db 1 aatccgagccatgtgtgaacgaagccagagaagaacagcagctcaacccctgtctgag 60
Qy 61 ggcagtgccagcagtggtgaggttccaaagatagttcgaatattccaccgggc 120
Db 61 ggcagtgccagcagtggtgaggttccaaagatagttcgaatattccaccgggc 120
Qy 121 ctggaacctgagcagtgagagactccggagagaagaatgagcgcgatgtgaatctgt 180
Db 121 ctggaacctgagcagtgagagactccggagagaagaatgagcgcgatgtgaatctgt 180
Qy 181 gacaagtgttctcccttggaattcttccctctcgaactgtgagggaggtcgaatctc 240
Db 181 gacaagtgttctcccttggaattcttccctctcgaactgtgagggaggtcgaatctc 240
Qy 241 atctcaaggtttacccggaatgagcagcagtggtcccccctacataagcgtgactgcac 300
Db 241 atctcaaggtttacccggaatgagcagcagtggtcccccctacataagcgtgactgcac 300
Qy 301 ccaagcagtgacctgtgtcagacaagaagagactctctcaatgatgatcgcacaacgcgc 360
Db 301 ccaagcagtgacctgtgtcagacaagaagagactctctcaatgatgatcgcacaacgcgc 360
Qy 361 gtgaactactgtgctgtgagagacatctctcaatgatgacctgtgcgtctgagag 420
Db 361 gtgaactactgtgctgtgagagacatctctcaatgatgacctgtgcgtctgagag 420
Qy 421 gagatccgggcatctgtcacaagaactaaagcagctgtgaggaacacatcagcgctg 480
Db 421 gagatccgggcatctgtcacaagaactaaagcagctgtgaggaacacatcagcgctg 480
Qy 481 cggggaagaccatgaagtgcacagtgaggagaggaugagagcttcaactcgaactg 540
Db 481 cggggaagaccatgaagtgcacagtgaggagaggaugagagcttcaactcgaactg 540
Qy 541 gacctgtgagagacatccgaagtgaattgttgactacttgcacatctgtgagcgagt 600
Db 541 gacctgtgagagacatccgaagtgaattgttgactacttgcacatctgtgagcgagt 600
Qy 601 taaccacaagccaccccccgaagcagggagctgtgagcgtgacacttgaagcacttgaagag 660
Db 601 taaccacaagccaccccccgaagcagggagctgtgagcgtgacacttgaagcacttgaagag 660
Qy 661 aaggtgtgtcgggagccgaattcatatcagcagcttcttcttgaggtcgaacatc 720
Db 661 aaggtgtgtcgggagccgaattcatatcagcagcttcttcttgaggtcgaacatc 720
Qy 721 ttccgcttctggaagcagatcacccgacatgagcacttgcacactgtcccatcgtcccgagatc 780
Db 721 ttccgcttctggaagcagatcacccgacatgagcacttgcacactgtcccatcgtcccgagatc 780
Qy 781 ttcccatcgaagcgtacacactcccttgcgacgttgaagctgtcccaacgtcgaggtg 840
Db 781 ttcccatcgaagcgtacacactcccttgcgacgttgaagctgtcccaacgtcgaggtg 840
Qy 841 ccacagagatcaagacgctgattgagccaatacaagaacaagatgtgcacccgaac 900
Db 841 ccacagagatcaagacgctgattgagccaatacaagaacaagatgtgcacccgaac 900
Qy 901 tatgcatcagctgtgcgctgtgagccttgcacagagcttctgcacatgtgctgtgagcca 960
Db 901 tatgcatcagctgtgcgctgtgagccttgcacagagcttctgcacatgtgctgtgagcca 960
Qy 961 ggcctcaacttcaacacctcaacccgagagatggtctacacaagaagtgtcgaagcgctg 1020
Db 961 ggcctcaacttcaacacctcaacccgagagatggtctacacaagaagtgtcgaagcgctg 1020
Qy 1021 gggatgtgagctgagagcccccagcgctccctacccctgaggtcctcaggtgcccccaag 1080
Db 1021 gggatgtgagctgagagcccccagcgctccctacccctgaggtcctcaggtgcccccaag 1080
Qy 1081 cgcgagaggaagatgagctcccatcttctgagcctccagacccaagaagttaacatctac 1140
Db 1081 cgcgagaggaagatgagctcccatcttctgagcctccagacccaagaagttaacatctac 1140
```

Db 1081 cgcgagagagatgatacgtccatcttcttgcgtccagaccagaagttacatctac 1140  
QY 1141 cgtaccagagatggagacagttccctaaagccgctggggacaattctctccctgccc 1200  
Db 1141 cgtaccagagatggagacagttccctaaagccgctggggacaattctctccctgccc 1200  
QY 1201 ttggggagacataagactactctcttctacgtgaagagaaagttccccaagagagag 1260  
Db 1201 ttggggagacataagactactctcttctacgtgaagagaaagttccccaagagagag 1260  
QY 1261 ctgctgaagatgtgggggagagagcttganacagtgaagcaagtgtcttgaagttctgt 1320  
Db 1261 ctgctgaagatgtgggggagagagcttganacagtgaagcaagtgtcttgaagttctgt 1320  
QY 1321 ctctccctctcgagagacccaacacggaatgttcaacaagtgaactgtccctccgagac 1380  
Db 1321 ctctccctctcgagagacccaacacggaatgttcaacaagtgaactgtccctccgagac 1380  
QY 1381 gatgaagcccttgcggtgagacccagcctgtgagagagagagctgtcggtggaacggc 1440  
Db 1381 gatgaagcccttgcggtgagacccagcctgtgagagagagagctgtcggtggaacggc 1440  
QY 1441 caggagatccctccacatcaactcaacagcccaacatcaacgggaaagccgtccctccgacccc 1500  
Db 1441 caggagatccctccacatcaactcaacagcccaacatcaacgggaaagccgtccctccgacccc 1500  
QY 1501 atcgtgggtctggggccccaagcggggtatgtcttccagaagagcctacttaagtttttc 1560  
Db 1501 atcgtgggtctggggccccaagcggggtatgtcttccagaagagcctacttaagtttttc 1560  
QY 1561 actcccgagagagacgggaaagcaactctctgaagtgctgaagaaagtaacgagtcctgggt 1620  
Db 1561 actcccgagagagacgggaaagcaactctctgaagtgctgaagaaagtaacgagtcctgggt 1620  
QY 1621 aattaccacacttgcatactggaaggtggaagaaacatccacacatgcccctgaactgacgacgg 1680  
Db 1621 aattaccacacttgcatactggaaggtggaagaaacatccacacatgcccctgaactgacgacgg 1680  
QY 1681 aatgctctcaacttggggacatcttcccttggcgagagatcatccagcccacagtaagtgt 1740  
Db 1681 aatgctctcaacttggggacatcttcccttggcgagagatcatccagcccacagtaagtgt 1740  
QY 1741 cccgtcagctcattgtcttggaaagacgagagccttggcctgtgagattgagcgggtggga 1800  
Db 1741 cccgtcagctcattgtcttggaaagacgagagccttggcctgtgagattgagcgggtggga 1800  
QY 1801 aagctgtatgagagagagagtcctccgtcccgacacatcatccagtaacttccagacacac 1860  
Db 1801 aagctgtatgagagagagagtcctccgtcccgacacatcatccagtaacttccagacacac 1860  
QY 1861 ttccctgtcaactgtgtgacaaatgacatcccaacttgcagaaactgtcttgcaggtgtgtg 1920  
Db 1861 ttccctgtcaactgtgtgacaaatgacatcccaacttgcagaaactgtcttgcaggtgtgtg 1920  
QY 1921 gaagacacattgagagcttctcaacagcccaacagaaatgagagaaacgagaggttcca 1980  
Db 1921 gaagacacattgagagcttctcaacagcccaacagaaatgagagaaacgagaggttcca 1980  
QY 1981 tgacctgtcttgcagcctgtcggttggagacacactgttccgcgcttccctccccaaca 2040  
Db 1981 tgacctgtcttgcagcctgtcggttggagacacactgttccgcgcttccctccccaaca 2040  
QY 2041 ggtgctgtcttcttggaaactcaactctctctgtcttctcccaacccggcctccactc 2100  
Db 2041 ggtgctgtcttcttggaaactcaactctctctgtcttctcccaacccggcctccactc 2100  
QY 2101 ccccaacttgcacatgagcagctagactgaggtgaggttcccaagccttccctggagacgtgag 2160  
Db 2101 ccccaacttgcacatgagcagctagactgaggtgaggttcccaagccttccctggagacgtgag 2160  
QY 2161 tcggcccaacatgggaactagttactcttctctcta 2196  
Db 2161 tcggcccaacatgggaactagttactcttctctcta 2196

RESULT 5  
US-09-802-640-33  
Sequence 33, Application US/09802640  
GENERAL INFORMATION:  
APPLICANT: Braun, Andreas  
APPLICANT: Bonsal Aruna  
APPLICANT: Kiehn Patrick  
TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH  
FILE REFERENCE: 24736-2048  
CURRENT APPLICATION NUMBER: US/09/802,640  
NUMBER OF SEQ ID NOS: 122  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 33  
LENGTH: 2196  
TYPE: DNA  
ORGANISM: Homo sapien  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (13)...(1983)  
OTHER INFORMATION: Nucleotide sequence encoding  
US-09-802-640-33  
5'-10-methylmetetrahydrofolate reductase (MTHFR)

Query Match 99.6%; Score 2186.6; DB 31; Length 2196;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 aattccgagacatggttgaacgagacgagaggaacagcagcctcaacccctgtggag 60  
Db 1 aattccgagacatggttgaacgagacgagaggaacagcagcctcaacccctgtggag 60  
QY 61 ggcaggtgcagcaggtgagcagtgagagatcccaagatagtcagagatgtccaccccgagc 120  
Db 61 ggcaggtgcagcaggtgagcagtgagagatcccaagatagtcagagatgtccaccccgagc 120  
QY 121 ctggacccctgagcagcatagagacatcccgagagaaatgagcggcgtatggaatcgtgt 180  
Db 121 ctggacccctgagcagcatagagacatcccgagagaaatgagcggcgtatggaatcgtgt 180  
QY 181 gacaaatgttctccctgtgaattctccctcctcgaactgtctgagagagctgtcaatctc 240  
Db 181 gacaaatgttctccctgtgaattctccctcctcgaactgtctgagagagctgtcaatctc 240  
QY 241 atctcaagtttggacggagatggcagcaggttggccctctataatgagctgtgacac 300  
Db 241 atctcaagtttggacggagatggcagcaggttggccctctataatgagctgtgacac 300  
QY 301 ccaagcaggtgacccctgtgctcaagaagagacatccctccatgatgatccgacacccc 360  
Db 301 ccaagcaggtgacccctgtgctcaagaagagacatccctccatgatgatccgacacccc 360  
QY 361 gtaactactgtggtgcttggagacatctctgtacatgacctgtgcctgaagcgtgtgag 420  
Db 361 gtaactactgtggtgcttggagacatctctgtacatgacctgtgcctgaagcgtgtgag 420  
QY 421 gagatcaaggccatctgcaacaagctgaagcagctgtggcctgtgaagaatacatatggcctg 480  
Db 421 gagatcaaggccatctgcaacaagctgaagcagctgtggcctgtgaagaatacatatggcctg 480  
QY 481 cgggagagcccaataatgtgacccagtgggaagagagagagaggttccaactaagcaggtg 540  
Db 481 cgggagagcccaataatgtgacccagtgggaagagagagagagaggttccaactaagcaggtg 540  
QY 541 gacctgtgtgaagacatcccgaaagtgaggttgggtacacttgcacatctgtgtgacaggt 600  
Db 541 gacctgtgtgaagacatcccgaaagtgaggttgggtacacttgcacatctgtgtgacaggt 600  
QY 601 taaccacaaggccaccccgaaagcagagagctttagagctgacactgaagcacttgaagag 660

```
Db 601 taccaccaagccaccccgaaagcaggagagcttgaggctgagcctggaagcattgaagag 660
Qy 661 aaggtgntgvcggagcagattcatcatcagcagagctttctcttgagctgaacattc 720
Db 661 aaggtgntgvcggagcagattcatcatcagcagagctttctcttgagctgaacattc 720
Qy 721 ttccgcttgtagagagcagatgacagagatgagcattgcccacatcgtcccgagtc 780
Db 721 ttccgcttgtagagagcagatgacagagatgagcattgcccacatcgtcccgagtc 780
Qy 781 ttccacatccagggctacacacccctcccgagcgttgtagagctgacagctgagagtg 840
Db 781 ttccacatccagggctacacacccctcccgagcgttgtagagctgacagctgagagtg 840
Qy 841 ccaagagagatcagagcagcgtgattgagcaatcaagaacacagatgctgcacatccgac 900
Db 841 ccaagagagatcagagcagcgtgattgagcaatcaagaacacagatgctgcacatccgac 900
Qy 901 tatgacatcgagctgagcgtgagcgttgccagagagcttgccagagcttgagctgagtc 960
Db 901 tatgacatcgagctgagcgtgagcgttgccagagagcttgccagagcttgagctgagtc 960
Qy 961 ggcctccacttctacacacccctcaaccccgagatggtacacacagagtgctgagagcg 1020
Db 961 ggcctccacttctacacacccctcaaccccgagatggtacacacagagtgctgagagcg 1020
Qy 1021 gggatgtgagctgagagcagcccgagcgtccctacaccccgagcttgagctgagtc 1080
Db 1021 gggatgtgagctgagagcagcccgagcgtccctacaccccgagcttgagctgagtc 1080
Qy 1081 cgcgcagagagagatgtagctccatctcttgagcctccagacaaagagttacatctac 1140
Db 1081 cgcgcagagagagatgtagctccatctcttgagcctccagacaaagagttacatctac 1140
Qy 1141 cgtacccaagagatgtagagagcttccctaagcgcgtgggagaaattccctccctgac 1200
Db 1141 cgtacccaagagatgtagagagcttccctaagcgcgtgggagaaattccctccctgac 1200
Qy 1201 ttggggagctgagagactactactctctctactctgaagagcagctccccaagagagag 1260
Db 1201 ttggggagctgagagactactactctctctactctgaagagcagctccccaagagagag 1260
Qy 1261 ctctctaaagatgtagggagagagcgtgancatgtagagcagtgctctgagagcttctgt 1320
Db 1261 ctctctaaagatgtagggagagagcgtgancatgtagagcagtgctctgagagcttctgt 1320
Qy 1321 cttaacctctgggagaaacaaacccgaaatggtcacaaagtactgctgagcctgagac 1380
Db 1321 cttaacctctgggagaaacaaacccgaaatggtcacaaagtactgctgagcctgagac 1380
Qy 1381 gatgagccctgtagcgtctgaagcagcgtctgtagagagagctgctgagtgagacgcg 1440
Db 1381 gatgagccctgtagcgtctgaagcagcgtctgtagagagagctgctgagtgagacgcg 1440
Qy 1441 caggggcatctacacatcaacacagcccaacatcaagggagaaacgctcccgagaccc 1500
Db 1441 caggggcatctacacatcaacacagcccaacatcaagggagaaacgctcccgagaccc 1500
Qy 1501 atcgtgagctgtagcccgagcggggtatgtctctcagaagagcctacttagagtttcc 1560
Db 1501 atcgtgagctgtagcccgagcggggtatgtctctcagaagagcctacttagagtttcc 1560
Qy 1561 attcccgagagacagcggaaagcactctgcaagtgcggaagaataagagctccgggtt 1620
Db 1561 attcccgagagacagcggaaagcactctgcaagtgcggaagaataagagctccgggtt 1620
Qy 1621 aattacacactgtcaatgtgaaggtgaaacacatcaccaatgcccctgagctgagcg 1680
Db 1621 aattacacactgtcaatgtgaaggtgaaacacatcaccaatgcccctgagctgagcg 1680
Qy 1681 aatgtgtcacttgtaggagattccctctgtagagagatcatccagccacgtagtgat 1740
Db 1681 aatgtgtcacttgtaggagattccctctgtagagagatcatccagccacgtagtgat 1740
```

```
Db 1681 aatgtgtcacttgtaggagattccctctgtagagagatcatccagccacgtagtgat 1740
Qy 1741 ccgctgagcttcatgtctctgtagagagagagccttgccctgtgagattgagcgttgagga 1800
Db 1741 ccgctgagcttcatgtctctgtagagagagagccttgccctgtgagattgagcgttgagga 1800
Qy 1801 aagctgtatgagagagagctcccgctcccgacacatcatccagttacatccagacattac 1860
Db 1801 aagctgtatgagagagagctcccgctcccgacacatcatccagttacatccagacattac 1860
Qy 1861 ttccgtgtaacctgtgtgagcaatgattcccatctgagacacatgctctcgtgagtggtg 1920
Db 1861 ttccgtgtaacctgtgtgagcaatgattcccatctgagacacatgctctcgtgagtggtg 1920
Qy 1921 gaagacacattgtagcttctcacaagcccaacccaatgtagagagaaacggagcttca 1980
Db 1921 gaagacacattgtagcttctcacaagcccaacccaatgtagagagaaacggagcttca 1980
Qy 1981 tgagcctgctgctgagcagccctgctgtagagcaatcctctgctccgctctctccaca 2040
Db 1981 tgagcctgctgctgagcagccctgctgtagagcaatcctctgctccgctctctccaca 2040
Qy 2041 gtgctgcttctcttggaactccactctctctgctgtctctccacaccccgctcattc 2100
Db 2041 gtgctgcttctcttggaactccactctctctgctgtctctccacaccccgctcattc 2100
Qy 2101 cccacactgacaaatgtagcagctagagctgtagagcttccagagcttctctgagcctgag 2160
Db 2101 cccacactgacaaatgtagcagctagagctgtagagcttccagagcttctctgagcctgag 2160
Qy 2161 tcggcccaatgtagagcagctagctctgtctctctctctctctctctctctctctct 2196
Db 2161 tcggcccaatgtagagcagctagctctgtctctctctctctctctctctctctctct 2196

RESULT 6
US-09-592-595-3
; Sequence 3, Application US/09592595
; GENERAL INFORMATION:
; APPLICANT: ROZEN, Rima
; TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE
; TITLE OF INVENTION: REDUCTASE AND USES THEREOF
; FILE REFERENCE: 04844/005005
; CURRENT APPLICATION NUMBER: US/09/592,595
; CURRENT FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: US 09/258,928
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: US 08/738,000
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: PCT/CA95/00314
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: GB 9410620.0
; PRIOR FILING DATE: 1994-05-26
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2219
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(1983)
US-09-592-595-3

Query Match 99.6% Score 2186.6 DB 22 Length 2219;
Best Local Similarity 99.7% Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```



QY 61 ggcacgtgcagacagtgacgtgacagctcccaagatagttcagagatgttccaccccgagc 120  
|||||  
Db 61 ggcacgtgcagacagtgacgtgacagctcccaagatagttcagagatgttccaccccgagc 120  
QY 121 ctggagccctgagcagcatgagagactccgggagaaagtgaagcggcggattggaatctgtg 180  
|||||  
Db 121 ctggagccctgagcagcatgagagactccgggagaaagtgaagcggcggattggaatctgtg 180  
QY 181 gacaaagtgttctccctctggaattcttccctccctcgcgaactgtctgagagagctgtcaatctc 240  
|||||  
Db 181 gacaaagtgttctccctctggaattcttccctccctcgcgaactgtctgagagagctgtcaatctc 240  
QY 241 atctcaagtttgagccggaatgacagcaggtgcccccttaacataagacgtgaactgtgac 300  
|||||  
Db 241 atctcaagtttgagccggaatgacagcaggtgcccccttaacataagacgtgaactgtgac 300  
QY 301 ccaagcaggtgacccctgtgtctcagacaaaggacacttccctcaatgatgtatcgccagacgcgc 360  
|||||  
Db 301 ccaagcaggtgacccctgtgtctcagacaaaggacacttccctcaatgatgtatcgccagacgcgc 360  
QY 361 gtgaaactctgtgacctgtgagagacacatccctcgaatcgtcgcgtcagcgcgtgag 420  
|||||  
Db 361 gtgaaactctgtgacctgtgagagacacatccctcgaatcgtcgcgtcagcgcgtgag 420  
QY 421 gagatcacggtccactctgtcacaaagctaaagcagctgagcctgagaaacatctagcgctgtg 480  
|||||  
Db 421 gagatcacggtccactctgtcacaaagctaaagcagctgagcctgagaaacatctagcgctgtg 480  
QY 481 cgggagagacccaataagtgacaaagtggagaaaggagagagagagcttcaactacgcagctg 540  
|||||  
Db 481 cgggagagacccaataagtgacaaagtggagaaaggagagagagagcttcaactacgcagctg 540  
QY 541 gacctgtgtgaagcacaatcccgaaagtgaatttgttgaactaacttggacatctgtgtgagcagt 600  
|||||  
Db 541 gacctgtgtgaagcacaatcccgaaagtgaatttgttgaactaacttggacatctgtgtgagcagt 600  
QY 601 taacccaaagggccaccccgaaagcagagagagcttgaaggctgacactgtgaagcacttgaagag 660  
|||||  
Db 601 taacccaaagggccaccccgaaagcagagagagcttgaaggctgacactgtgaagcacttgaagag 660  
QY 661 aaggtgtgttcggagacagattcatcatcacagagacttcttcttgaggtctgaaacatctc 720  
|||||  
Db 661 aaggtgtgttcggagacagattcatcatcacagagacttcttcttgaggtctgaaacatctc 720  
QY 721 ttccggtctgtgaaagcactgacacgcagacatgaggtgacatctgtgcccacgtcccccagatc 780  
|||||  
Db 721 ttccggtctgtgaaagcactgacacgcagacatgaggtgacatctgtgcccacgtcccccagatc 780  
QY 781 ttcccccatacagggtctaacacatcccttcggcagactgttgaagctgtccaaagtggaggtg 840  
|||||  
Db 781 ttcccccatacagggtctaacacatcccttcggcagactgttgaagctgtccaaagtggaggtg 840  
QY 841 ccaacagagagatacaagagcgtgtgattgagccaataaagacacagatgctgtgcatccgcaac 900  
|||||  
Db 841 ccaacagagagatacaagagcgtgtgattgagccaataaagacacagatgctgtgcatccgcaac 900  
QY 901 taagagatcgaggttgagcgtgtgagccctgtgacagagacttctgagcagctgtgctgtgagca 960  
|||||  
Db 901 taagagatcgaggttgagcgtgtgagccctgtgagcagagacttctgagcagctgtgctgtgagca 960  
QY 961 ggcctcactcttatacacccttcaaccgcgagatgtgtacccaagaagttgttgaagcgctg 1020  
|||||  
Db 961 ggcctcactcttatacacccttcaaccgcgagatgtgtacccaagaagttgttgaagcgctg 1020  
QY 1021 gggatgtgagctgagagaccccgagcggtcccttaaccctgtcgctctcagttgcccacccaag 1080  
|||||  
Db 1021 gggatgtgagctgagagaccccgagcggtcccttaaccctgtcgctctcagttgcccacccaag 1080  
QY 1081 cgcgcagagaaagatgtatgctccatctctctgtgaccttccagacaaagaggttaacatctac 1140  
|||||  
Db 1081 cgcgcagagaaagatgtatgctccatctctctgtgaccttccagacaaagaggttaacatctac 1140  
QY 1141 cgtaccagagagtgagacagatctccctaacggcgctggggaattcccttcccttgc 1200  
|||||

Db 1141 cgtaccagagagtgagacagatctccctaacggcgctggggaattcccttcccttgc 1200  
QY 1201 ttggggagctggaagagactaactaactcttcaactgaaagacaaagtcccccagaagagag 1260  
|||||  
Db 1201 ttggggagctggaagagactaactaactcttcaactgaaagacaaagtcccccagaagagag 1260  
QY 1261 ctgctgaaagatgtgagggagagctgancagtgaaagaaagtgtcttgnaaagttctgtct 1320  
|||||  
Db 1261 ctgctgaaagatgtgagggagagagctgaaacagtgaaagaaagtgtcttgnaaagttctgtct 1320  
QY 1321 cttaactctcggagagaaacccaacgggaatggttcaacaagaagtgtctgtccctgtgac 1380  
|||||  
Db 1321 cttaactctcggagagaaacccaacgggaatggttcaacaagaagtgtctgtccctgtgac 1380  
QY 1381 gataagcccttgagagagctgagacagacactgtctgaaagagagagctgtctgtgggtgaa 1440  
|||||  
Db 1381 gataagcccttgagagagctgagacagacactgtctgaaagagagagctgtctgtgggtgaa 1440  
QY 1441 cagggcatactcacaacatacacaacccaacccaacccaacccaacccaacccaacccaaccc 1500  
|||||  
Db 1441 cagggcatactcacaacatacacaacccaacccaacccaacccaacccaacccaacccaaccc 1500  
QY 1501 atcgtgagctgagggccccaagcgaggtatgtcttccagaagagcttaagagttttc 1560  
|||||  
Db 1501 atcgtgagctgagggccccaagcgaggtatgtcttccagaagagcttaagagttttc 1560  
QY 1561 acttcccgagagacagagagacacttctgcaaggtgtctgaaagaaagtacgagctccgggtt 1620  
|||||  
Db 1561 acttcccgagagacagagagacacttctgcaaggtgtctgaaagaaagtacgagctccgggtt 1620  
QY 1621 aattaaccaacttgcataatgtgaaggggtgaaaaacatacacaatgcccctgtgaagcgcg 1680  
|||||  
Db 1621 aattaaccaacttgcataatgtgaaggggtgaaaaacatacacaatgcccctgtgaagcgcg 1680  
QY 1681 aatgtctgacacttggggacacttccctggcgagagatacatccagcccacgtaatgtgat 1740  
|||||  
Db 1681 aatgtctgacacttggggacacttccctggcgagagatacatccagcccacgtaatgtgat 1740  
QY 1741 cccgtcaagcttcatgttctggaagagacagagccttctgcccctgtgagattgagcggtggga 1800  
|||||  
Db 1741 cccgtcaagcttcatgttctggaagagacagagccttctgcccctgtgagattgagcggtggga 1800  
QY 1801 aagctgtatgagagagaggttcccggtcccgacacatcatccagttacatccagacaactac 1860  
|||||  
Db 1801 aagctgtatgagagagaggttcccggtcccgacacatcatccagttacatccagacaactac 1860  
QY 1861 ttccgtgtaacacctgtggaacaatgacttcccactggaacactgtgcccctgtgacaggtgtg 1920  
|||||  
Db 1861 ttccgtgtaacacctgtggaacaatgacttcccactggaacactgtgcccctgtgacaggtgtg 1920  
QY 1921 gaaagacacattggaacttctcaacagggcccaacccaagaatgacgagaaacggaaggttcca 1980  
|||||  
Db 1921 gaaagacacattggaacttctcaacagggcccaacccaagaatgacgagaaacggaaggttcca 1980  
QY 1981 tgaacctgtgtcttgaacggcctgtggaagcaacttcttccggttcccttccctccca 2040  
|||||  
Db 1981 tgaacctgtgtcttgaacggcctgtggaagcaacttcttccggttcccttccctccca 2040  
QY 2041 gtgctgtctctcttgggaaactcaacttctctctgtctcttcccaaccccgagctccacat 2100  
|||||  
Db 2041 gtgctgtctctcttgggaaactcaacttctctctgtctcttcccaaccccgagctccacat 2100  
QY 2101 gccacactgaaacatgagcagctgagatgagatgagagcttccagagcttccctgtgagcctgag 2160  
|||||  
Db 2101 gccacactgaaacatgagcagctgagatgagatgagagcttccagagcttccctgtgagcctgag 2160  
QY 2161 tcggcccacatggaacatactactctctctca 2196  
|||||  
Db 2161 tcggcccacatggaacatactactctctctca 2196

RESULT 7



US-09-592-595A-3  
; Sequence 3, Application US/09592595A  
; GENERAL INFORMATION:  
; APPLICANT: ROZEN, Rima  
; TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE  
; FILE REFERENCE: REDUCTASE AND USES THEREOF  
; CURRENT APPLICATION NUMBER: US/09/592,595A  
; PRIORITY FILING DATE: 2000-06-12  
; PRIORITY FILING DATE: 1999-03-01  
; PRIORITY FILING DATE: 1997-02-12  
; PRIORITY FILING DATE: 1995-05-25  
; PRIORITY FILING DATE: 1994-05-26  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO: 3  
; LENGTH: 2219  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (13)...(1983)  
US-09-592-595A-3

Query Match 99.6% Score 2186.6; DB 22; Length 2219;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 aattccgagcattggtgaaacgaagaaacagacagcccaacccctgttgag 60  
Db 1 aattccgagcattggtgaaacgaagaaacagacagcccaacccctgttgag 60  
QY 61 ggcagctccagcagtgagcagtgaaagctccaagaatagttcgaga 120  
Db 61 ggcagctccagcagtgagcagtgaaagctccaagaatagttcgaga 120  
QY 121 ctgagaccctgagcgagcctgagagacctccgagagagatgagcgagattcgatc 180  
Db 121 ctgagaccctgagcgagcctgagagacctccgagagagatgagcgagattcgatc 180  
QY 181 gacaaagtgcttcctccctggaattcttcctccctcctcgaactgtagggagctgtcaatc 240  
Db 181 gacaaagtgcttcctccctggaattcttcctccctcctcgaactgtagggagctgtcaatc 240  
QY 241 atctcaaggtttgacccgagatgagcagtggtgccccctctacataagacgtgacctggac 300  
Db 241 atctcaaggtttgacccgagatgagcagtggtgccccctctacataagacgtgacctggac 300  
QY 301 cccgagcagtgagcctgctcagacaaaggagacccctcctcagatgatacgccagacagcc 360  
Db 301 cccgagcagtgagcctgctcagacaaaggagacccctcctcagatgatacgccagacagcc 360  
QY 361 gtgaaactactgtgctcgtgagacatccctgacatgacccgtgcgcgttaagcgcccgag 420  
Db 361 gtgaaactactgtgctcgtgagacatccctgacatgacccgtgcgcgttaagcgcccgag 420  
QY 421 gagatacagggcactcgtcgaacaaagctaacgacgtgagctgagagacatcatctgctg 480  
Db 421 gagatacagggcactcgtcgaacaaagctaacgacgtgagctgagagacatcatctgctg 480  
QY 481 cgggagacccaataagtgaaacagtgaggagagagagagagagagagagagagagagagag 540  
Db 481 cgggagacccaataagtgaaacagtgaggagagagagagagagagagagagagagagagag 540  
QY 541 gacctgtgtgaaacacatccgaaagtgtgtgtgactactgtgacatctgtgtgagaggt 600  
Db 541 gacctgtgtgaaacacatccgaaagtgtgtgtgactactgtgacatctgtgtgagaggt 600

QY 601 taaccacaaagccaccccgaaagcagtgagcttggagctgacgtgaagcacttgaaagag 660  
Db 601 taaccacaaagccaccccgaaagcagtgagcttggagctgacgtgaagcacttgaaagag 660  
QY 661 aagtgcttcgagagacagcattcaatcaacagcagcttcttggagctgacacatc 720  
Db 661 aagtgcttcgagagacagcattcaatcaacagcagcttcttggagctgacacatc 720  
QY 721 ttccgcttggagagcagtcagacagcagcagcagcagcagcagcagcagcagcagcagc 780  
Db 721 ttccgcttggagagcagtcagacagcagcagcagcagcagcagcagcagcagcagcagc 780  
QY 781 ttccacacagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 840  
Db 781 ttccacacagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 840  
QY 841 ccacagagagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 900  
Db 841 ccacagagagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 900  
QY 901 tatgcatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 960  
Db 901 tatgcatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 960  
QY 961 ggcctcacttctacacccctcaacccgagatgtgtacacagagtgctgaaagcgctg 1020  
Db 961 ggcctcacttctacacccctcaacccgagatgtgtacacagagtgctgaaagcgctg 1020  
QY 1021 gggatgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1080  
Db 1021 gggatgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1080  
QY 1081 cgcagagagagagatgtaagctccatctctgtgagcctcagaccaaagagttacatctac 1140  
Db 1081 cgcagagagagagatgtaagctccatctctgtgagcctcagaccaaagagttacatctac 1140  
QY 1141 cgtacccaagagtgagacagtgctccctaaacggcgtctggagacattccctcctgac 1200  
Db 1141 cgtacccaagagtgagacagtgctccctaaacggcgtctggagacattccctcctgac 1200  
QY 1201 ttggggagcctgaaagactacacctctctacactgaaagagcaagctccccaagagagag 1260  
Db 1201 ttggggagcctgaaagactacacctctctacactgaaagagcaagctccccaagagagag 1260  
QY 1261 ctgctaaagatgtggggagagagagcagtgaaagcagtgctctgaaagctcttct 1320  
Db 1261 ctgctaaagatgtggggagagagagcagtgaaagcagtgctctgaaagctcttct 1320  
QY 1321 cttaacctctggagaaaccaaaccgaaatggtcaacaagctgactgtgacctggaac 1380  
Db 1321 cttaacctctggagaaaccaaaccgaaatggtcaacaagctgactgtgacctggaac 1380  
QY 1381 gttgaagcccttgaggcttgaagccagcctgctgaaagagagcctgctgggtgaaacgc 1440  
Db 1381 gttgaagcccttgaggcttgaagccagcctgctgaaagagagcctgctgggtgaaacgc 1440  
QY 1441 cgggagcactcctacacatcaacacacagccacacacacacacacacacacacacacacac 1500  
Db 1441 cgggagcactcctacacatcaacacacagccacacacacacacacacacacacacacacac 1500  
QY 1501 atcgtgagctggggcccgagcagtgctatgtcttcagaaagcctacttaagttttc 1560  
Db 1501 atcgtgagctggggcccgagcagtgctatgtcttcagaaagcctacttaagttttc 1560  
QY 1561 acttcccgagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1620  
Db 1561 acttcccgagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1620  
QY 1621 aattacacactgtcaatgtgaaggtgaaacacatcaacaaatgcccctgaaactgacagcg 1680  
Db 1621 aattacacactgtcaatgtgaaggtgaaacacatcaacaaatgcccctgaaactgacagcg 1680  
QY 1681 aatgtgtcacttggggcacttctccctggggcgagagatcaacacagcccaacgctagtgat 1740

Db 1681 aatgctgtaacttgggacgtctcttccctgggcagagatcatccacgcccagtaatgagat 1740  
QY 1741 cccgtcagcttcatcttctggaagacagagccttggccctttagattgagcggtgggga 1800  
Db 1741 cccgtcagcttcatcttctggaagacagagccttggccctttagattgagcggtgggga 1800  
QY 1801 aagctgtatgagagagagtcctccgtccgcagacatcatccagtaacatccacgacaactac 1860  
Db 1801 aagctgtatgagagagagtcctccgtccgcagacatcatccagtaacatccacgacaactac 1860  
QY 1861 ttcctggtcaacctggtggagacatgacttccactgagacaaatgctctgtgagatgtgtg 1920  
Db 1861 ttcctggtcaacctggtggagacatgacttccactgagacaaatgctctgtgagatgtgtg 1920  
QY 1921 gaagacacattgagacttctcaacagcgcacacacgaatgagagaaacgagacttca 1980  
Db 1921 gaagacacattgagacttctcaacagcgcacacacgaatgagagaaacgagacttca 1980  
QY 1981 tgacctgtcgtcttgagacgcttccgtggttggagacatctctgtccgccttccctccaca 2040  
Db 1981 tgacctgtcgtcttgagacgcttccgtggttggagacatctctgtccgccttccctccaca 2040  
QY 2041 gtgtcgtctctcttggagac 2100  
Db 2041 gtgtcgtctctcttggagac 2100  
QY 2101 ccccaacctggaatgagcagctagactgagatgaggtcttcagagctcttcttcagactgag 2160  
Db 2101 ccccaacctggaatgagcagctagactgagatgaggtcttcagagctcttcttcagactgag 2160  
QY 2161 tcggccccacatgggaacctagtaactctctctcta 2196  
Db 2161 tcggccccacatgggaacctagtaactctctctcta 2196

RESULT 8  
US-09-660-872-3  
: Sequence 3, Application US/09660872  
: GENERAL INFORMATION:  
: APPLICANT: ROZEN, Rima  
: APPLICANT: COLETTE, Philippe  
: TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE  
: FILE REFERENCE: 04844/005004  
: CURRENT APPLICATION NUMBER: US/09/660, 872  
: PRIOR FILING DATE: 2000-09-13  
: PRIOR APPLICATION NUMBER: GB 9410620.0  
: PRIOR FILING DATE: 1994-05-26  
: PRIOR APPLICATION NUMBER: US 08/738, 000  
: PRIOR FILING DATE: 1997-02-12  
: PRIOR APPLICATION NUMBER: US 09/258, 928  
: PRIOR FILING DATE: 1999-03-01  
: NUMBER OF SEQ ID NOS: 14  
: SOFTWARE: FASTSEQ for Windows Version 4.0  
: SEQ ID NO 3  
: LENGTH: 2219  
: TYPE: DNA  
: ORGANISM: Homo sapiens  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: (13)...(1983)  
US-09-660-872-3

Query Match 99.6%; Score 2186.6; DB 26; Length 2219;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 aatccgagcagcatggtgaacgaagccagaggaacagacagcctcaacccctgcttggag 60  
Db 1 aatccgagcagcatggtgaacgaagccagaggaacagacagcctcaacccctgcttggag 60

QY 61 ggcagtgccagagagtgagcagtgagagcttccaaagatgttcgagatgttccacccgggc 120  
Db 61 ggcagtgccagagagtgagcagtgagagcttccaaagatgttcgagatgttccacccgggc 120  
QY 121 ctgagacccctgagcggcagatgagagactccgggaggaatgaaagcggcagcttggaatctgt 180  
Db 121 ctgagacccctgagcggcagatgagagactccgggaggaatgaaagcggcagcttggaatctgt 180  
QY 181 gacaaagtgttctcccttggaattcttccctccgtaactgtcagggagagctgtcaatctc 240  
Db 181 gacaaagtgttctcccttggaattcttccctccgtaactgtcagggagagctgtcaatctc 240  
QY 241 atctcaagtttgagccgagatgagcagaggttggcccccctacatagatgagtgacttgagac 300  
Db 241 atctcaagtttgagccgagatgagcagaggttggcccccctacatagatgagtgacttgagac 300  
QY 301 ccaagcaggtgacccctggtctcagacaaagagacacttccatgatatcgcacagacgcgc 360  
Db 301 ccaagcaggtgacccctggtctcagacaaagagacacttccatgatatcgcacagacgcgc 360  
QY 361 gtgaaactactgtgagccttgagagacacatccctgacatgacttgcgcgtcagagcgcgtgag 420  
Db 361 gtgaaactactgtgagccttgagagacacatccctgacatgacttgcgcgtcagagcgcgtgag 420  
QY 421 gagaatcagggccactctgcacaaagctaaagcagctggtggtcggaggaacatcatgtgcgtg 480  
Db 421 gagaatcagggccactctgcacaaagctaaagcagctggtggtcggaggaacatcatgtgcgtg 480  
QY 481 cggggagagcccaatagatgagacacatgaggaagagagagagagagagagagagagagagag 540  
Db 481 cggggagagcccaatagatgagacacatgaggaagagagagagagagagagagagagagagag 540  
QY 541 gacctgtgaaagcagacatcccgaaagtgtgtgtacttaacttggacatctgtgtgtgcaggt 600  
Db 541 gacctgtgaaagcagacatcccgaaagtgtgtgtacttaacttggacatctgtgtgtgcaggt 600  
QY 601 taaccaaaagggcaccaccccgaaagcagagagcttggaggtgcagctgaaagcacttgaagag 660  
Db 601 taaccaaaagggcaccaccccgaaagcagagagcttggaggtgcagctgaaagcacttgaagag 660  
QY 661 aaggtgtgtcgggagagcagatttcatcatcagcagagcttcttctgtggtctgacacatc 720  
Db 661 aaggtgtgtcgggagagcagatttcatcatcagcagagcttcttctgtggtctgacacatc 720  
QY 721 ttccgcttgtgaaagagatgacacccagatgagatgagacacttggccacacgctcccgagatc 780  
Db 721 ttccgcttgtgaaagagatgacacccagatgagatgagacacttggccacacgctcccgagatc 780  
QY 781 ttccacatcagaggtctacacactccctcggcagagctgtgaaagctgtccaaagctggaggtg 840  
Db 781 ttccacatcagaggtctacacactccctcggcagagctgtgaaagctgtccaaagctggaggtg 840  
QY 841 ccaagagagatcaagagcgtgattgagacacatcaaaagacagatgtgtccacacgcaac 900  
Db 841 ccaagagagatcaagagcgtgattgagacacatcaaaagacagatgtgtccacacgcaac 900  
QY 901 tatgacatcgagctgagcgtgagcctgtgccaagagcttccagcagtggtctgtgtgca 960  
Db 901 tatgacatcgagctgagcgtgagcctgtgccaagagcttccagcagtggtctgtgtgca 960  
QY 961 ggcctcaactctacacccctcaaccccgagatgagcttaccacaaaggtgtctgaaagcgctg 1020  
Db 961 ggcctcaactctacacccctcaaccccgagatgagcttaccacaaaggtgtctgaaagcgctg 1020  
QY 1021 gggagtgagacttgagagcccaagcgctccctcactcgtctcagtgccaccccaag 1080  
Db 1021 gggagtgagacttgagagcccaagcgctccctcactcgtctcagtgccaccccaag 1080  
QY 1081 cggcagagagagagatgagctccatctctgggctccagacaaagaggttacctac 1140  
Db 1081 cggcagagagagagatgagctccatctctgggctccagacaaagaggttacctac 1140  
QY 1141 cgtaccagagagtgagagaggttccctaacgacgctgtgggaattccctccctcgtcc 1200

```
Db 1141 cgtaccagagatgagcagctcccaacgycgctgagcacttccctccctgc 1200
QY 1201 ttctggagagctgaagactactactcttactctgaagcgaagtcctcccaagagag 1260
Db 1201 ttctggagagctgaagactactactcttactctgaagcgaagtcctcccaagagag 1260
QY 1261 ctctctgaagatctgagggagagcctgaanacatgaagcaagctctctgaagcttctgt 1320
Db 1261 ctctctgaagatctgagggagagcctgaanacatgaagcaagctctctgaagcttctgt 1320
QY 1321 ctttaacctctcgagagacccaacccggaatggtcacaanaatgtactgctcgccctgaaac 1380
Db 1321 ctttaacctctcgagagacccaacccggaatggtcacaanaatgtactgctcgccctgaaac 1380
QY 1381 gatgaagccctgagcagctgaagcagcctgctgaagagagagctgctgagctgaacccg 1440
Db 1381 gatgaagccctgagcagctgaagcagcctgctgaagagagagctgctgagctgaacccg 1440
QY 1441 cagggacatctctccatcaactacacagcccaacatcaacagcggaagccgtctccgaccc 1500
Db 1441 cagggacatctctccatcaactacacagcccaacatcaacagcggaagccgtctccgaccc 1500
QY 1501 atcgtgagctgagggcccaagcgggagctatgctctcagaagcctactagaattttc 1560
Db 1501 atcgtgagctgagggcccaagcgggagctatgctctcagaagcctactagaattttc 1560
QY 1561 acttcccgagagacagcggagagactctgcaagctgctgaagaagtaagcagctccgggtc 1620
Db 1561 acttcccgagagacagcggagagactctgcaagctgctgaagaagtaagcagctccgggtc 1620
QY 1621 aattacaaccttgcataatgagaggtgaaatacatcaacacatccctgaactgacagccg 1680
Db 1621 aattacaaccttgcataatgagaggtgaaatacatcaacacatccctgaactgacagccg 1680
QY 1681 aatgctgctactctgggagcatcttccctgagcgagagatcatccagcccaacagtaagat 1740
Db 1681 aatgctgctactctgggagcatcttccctgagcgagagatcatccagcccaacagtaagat 1740
QY 1741 cccgtaagcttcatgtctgaaagacgagagccttggccctgtaagattgaagcggtggga 1800
Db 1741 cccgtaagcttcatgtctgaaagacgagagccttggccctgtaagattgaagcggtggga 1800
QY 1801 aagctgtatgagagagaggtcccgctccgacacatcatccagtaacatccagcaactaac 1860
Db 1801 aagctgtatgagagagaggtcccgctccgacacatcatccagtaacatccagcaactaac 1860
QY 1861 ttctctgtcaaacctgtgtaacaaatgacttccacttgaacactgctctgagcaggtgtg 1920
Db 1861 ttctctgtcaaacctgtgtaacaaatgacttccacttgaacactgctctgagcaggtgtg 1920
QY 1921 gaagacacatgagagcttctcaacagcccaacccaagaatgacgagaaacgagagcttca 1980
Db 1921 gaagacacatgagagcttctcaacagcccaacccaagaatgacgagaaacgagagcttca 1980
QY 1981 tgaacctggtctctgagcagcctgctgtgagcgaactctgtcccgctctctctccaca 2040
Db 1981 tgaacctggtctctgagcagcctgctgtgagcgaactctgtcccgctctctctccaca 2040
QY 2041 gtgctgtctctcttggaaactccactctctctgtctctcccaacccgagctccacac 2100
Db 2041 gtgctgtctctcttggaaactccactctctctgtctctcccaacccgagctccacac 2100
QY 2101 ccccaactgacaaatgacagctagactgaggttcaagctctctctgagcactgag 2160
Db 2101 ccccaactgacaaatgacagctagactgaggttcaagctctctctgagcactgag 2160
QY 2161 tcggccccacatgagaaactagtaactctctgtctca 2196
Db 2161 tcggccccacatgagaaactagtaactctctgtctca 2196
```

RESULT 9

```
US-09-660-872A-3
; Sequence 3, Application US/09660872A
; GENERAL INFORMATION:
; APPLICANT: ROZEN, Rima
; TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
; FILE REFERENCE: 04844/005004
; CURRENT APPLICATION NUMBER: US/09/660, 872A
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/IB00/00442
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/258, 928
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: US 08/738, 000
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: PCT/CA95/00314
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: GB 9410620.0
; PRIOR FILING DATE: 1994-05-26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 2219
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)...(1983)
US-09-660-872A-3
```

```
Query Match 99.6%; Score 2186.6; DB 26; Length 2219;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 aattccgagagcatgtgtgacgaagccagaggaacacagacgctcaacccctgttgaag 60
Db 1 aattccgagagcatgtgtgacgaagccagaggaacacagacgctcaacccctgttgaag 60
QY 61 ggcagtgccagcagtgagcagtgagagctccaaagatgttcgagatgttccaccccgagc 120
Db 61 ggcagtgccagcagtgagcagtgagagctccaaagatgttcgagatgttccaccccgagc 120
QY 121 ctggacccctgagcagcatagagagactccggaggaagatgagcgagcttggaaatctgt 180
Db 121 ctggacccctgagcagcatagagagactccggaggaagatgagcgagcttggaaatctgt 180
QY 181 gacaagtggtctccctggaattcttccctccgaactgctgaaagagagctgtaactctc 240
Db 181 gacaagtggtctccctggaattcttccctccgaactgctgaaagagagctgtaactctc 240
QY 241 atcttaaggtttgacccgagatgagcagaggtgagccctctacataagacgtgactgac 300
Db 241 atcttaaggtttgacccgagatgagcagaggtgagccctctacataagacgtgactgac 300
QY 301 ccagcaggtgacccctggtctcagaagaagagacctctctcatgatgatgacgacagcc 360
Db 301 ccagcaggtgacccctggtctcagaagaagagacctctctcatgatgatgacgacagcc 360
QY 361 gtgaactactgtgctgagagacacatctctgacatgacctgctgcgctcagcgctgag 420
Db 361 gtgaactactgtgctgagagacacatctctgacatgacctgctgcgctcagcgctgag 420
QY 421 gagatcaaggggccatcttcacaaagctgaagcctgagcctggaagaacatcatgtgcctg 480
Db 421 gagatcaaggggccatcttcacaaagctgaagcctgagcctggaagaacatcatgtgcctg 480
QY 481 cgggagagacccaatagtgacacagtgaggaaagagagagagagcttcaactaagcagtg 540
Db 481 cgggagagacccaatagtgacacagtgaggaaagagagagagagcttcaactaagcagtg 540
QY 541 gactcgtgtaagcacatccgaagtgagtttggtaactacttgaacatctgtgtgagcagt 600
```

```
Db 541 gactgtgtgaagcacatccgaagtgtgtgtactacttctgacatctgtgtgcaagt 600
QY 601 taaccacaaggccaccccgaaagcagtgagcttctgagcttgcacccaagcatttaagag 660
Db 601 taaccacaaggccaccccgaaagcagtgagcttctgagcttgcacccaagcatttaagag 660
QY 661 aaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720
Db 661 aaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720
QY 721 ttcggctgtgtgaagcagatgcacgacatgagcagatgcacgacatgcacgacatgcacg 780
Db 721 ttcggctgtgtgaagcagatgcacgacatgagcagatgcacgacatgcacgacatgcacg 780
QY 781 tttcccatcagaagctacacacacacacacacacacacacacacacacacacacacacac 840
Db 781 tttcccatcagaagctacacacacacacacacacacacacacacacacacacacacacac 840
QY 841 ccaacaagaagatcaagaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 900
Db 841 ccaacaagaagatcaagaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 900
QY 901 tatgtgacatcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 960
Db 901 tatgtgacatcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 960
QY 961 ggcctcactctacacacacacacacacacacacacacacacacacacacacacacacac 1020
Db 961 ggcctcactctacacacacacacacacacacacacacacacacacacacacacacacac 1020
QY 1021 gggatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1080
Db 1021 gggatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1080
QY 1081 cgcgcgaagaagaatgtacgtccatctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1140
Db 1081 cgcgcgaagaagaatgtacgtccatctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1140
QY 1141 cgtaccagaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1200
Db 1141 cgtaccagaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1200
QY 1201 tttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1260
Db 1201 tttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1260
QY 1261 ctgtgtgaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1320
Db 1261 ctgtgtgaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1320
QY 1321 ctttaacctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1380
Db 1321 ctttaacctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1380
QY 1381 gatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440
Db 1381 gatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1440
QY 1441 caggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1500
Db 1441 caggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1500
QY 1501 atcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1560
Db 1501 atcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1560
QY 1561 acttcccgagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1620
Db 1561 acttcccgagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1620
QY 1621 aattacaacctgtcaatgtgaaggtgaagaacatcaacatgcccctgagctgagcagcg 1680
Db 1621 aattacaacctgtcaatgtgaaggtgaagaacatcaacatgcccctgagctgagcagcg 1680
```

```
Db 1621 aattacaacctgtcaatgtgaaggtgaagaacatcaacatgcccctgagctgagcagcg 1680
QY 1681 aatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1740
Db 1681 aatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1740
QY 1741 cccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1800
Db 1741 cccgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1800
QY 1801 aagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1860
Db 1801 aagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1860
QY 1861 tttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1920
Db 1861 tttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1920
QY 1921 gaagacacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1980
Db 1921 gaagacacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1980
QY 1981 tgaacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2040
Db 1981 tgaacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2040
QY 2041 gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2100
Db 2041 gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2100
QY 2101 ccccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2160
Db 2101 ccccactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2160
QY 2161 tcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2196
Db 2161 tcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2196
```

```
RESULT 10
US-09-728-910-3
; Sequence 3, Application US/09728910
; GENERAL INFORMATION:
; APPLICANT: Rozen, Rima
; TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE
; FILE REFERENCE: 04844/006001
; CURRENT APPLICATION NUMBER: US/09/728,910
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/258,928
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2219
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13) ... (1983)
US-09-728-910-3
```

```
Query Match 99.6%; Score 2186.6; DB 29; Length 2219;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 aatccggagcagtggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 60
Db 1 aatccggagcagtggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 60
QY 61 ggcagtgccagcagtgagcagtgagcagcagcagcagcagcagcagcagcagcagcagcagc 120
```

Db	1141	cgtaaccaggaatgaggagaggtctccctaaacgagccgtctgggacaaattccctctccctctgc	1200
QY	1201	tttgaggagctgaaagagactactaccctctctactctgaaagagcaagctccccaagagagag	1260
Db	1201	tttgaggagctgaaagagactactaccctctctctactctgaaagagcaagctccccaagagagag	1260
QY	1261	ctgcgcgaagatgtgggggagagagctgacnagctgaaagaaatgctcttngaaagctttgtc	1320
Db	1261	ctgcgcgaagatgtgggggagagagctgacnagctgaaagaaatgctcttngaaagctttgtc	1320
QY	1321	cttaacctctcgggagaaaccaacggaatggtacaaagatgactctgcctccctggagac	1380
Db	1321	cttctccctctcgggagaaaccaacggaatggtacaaagatgactctgcctccctggagac	1380
QY	1381	gatgagccccctggcgctgtagaaccagagctctgtaagagagagctgcgcgggtgtaaccgc	1440
Db	1381	gatgagccccctggcgctgtagaaccagagctctgtaagagagagctgcgcgggtgtaaccgc	1440
QY	1441	caggagcatctccatccatcaactccaaagcccaacatccaaacggaagacggtctccgaaccc	1500
Db	1441	caggagcatctccatccatccatcaactccaaagcccaacatccaaacggaagacggtctccgaaccc	1500
QY	1501	atcgttgagctgggcccccaacgaggggtatgctctccagaagagccctaaagcttttc	1560
Db	1501	atcgttgagctgggcccccaacgaggggtatgctctccagaagagccctaaagagcttttc	1560
QY	1561	actcccgcgagacagcggagacattctgcaagtgctgaaagagatagagctcccggtc	1620
Db	1561	actcccgcgagacagcggagacattctgcaagtgctgaaagagatagagctcccggtc	1620
QY	1621	aattacaacctgtgcaatgtgaaagggttgaaanaatacaaatgccccctgaactgcagacg	1680
Db	1621	aattacaacctgtgcaatgtgaaagggttgaaanaatacaaatgccccctgaactgcagacg	1680
QY	1681	aatgctgtaacctggggacatctctcccttgggcggaagatcatccacgaccgtaagtgtat	1740
Db	1681	aatgctgtaacctggggacatctctcccttgggcggaagatcatccacgaccgtaagtgtat	1740
QY	1741	cccgctcagctcaatgtctctgaaaggacagagagcccttggccctgtgaagttagagcggtgggaa	1800
Db	1741	cccgctcagctcaatgtctctgaaaggacagagagcccttggccctgtgaagttagagcggtgggaa	1800
QY	1801	aagctgtatagaggagagagctcccgctccgacacatcatccaaatataccacagacaactaac	1860
Db	1801	aagctgtatagaggagagagctcccgctccgacacatcatccaaatataccacagacaactaac	1860
QY	1861	ttcctgtgtaaaccttggtagaacaatgactccccactggaanaactgctctgacaggtgtg	1920
Db	1861	ttcctgtgtaaaccttggtagaacaatgactccccactggaanaactgctctgacaggtgtg	1920
QY	1921	gaagacacatlggaagctcttcaacacagcccaacccaagaaatgcgaaagaaacggaggtcca	1980
Db	1921	gaagacacacatlggaagctcttcaacacagcccaacccaagaaatgcgaaagaaacggaggtcca	1980
QY	1981	tgaacctggtctctatagacgcccgtgttgagagcaactctgtctccgctctctctccaca	2040
Db	1981	tgaacctggtctctatagacgcccgtgttgagagcaactctgtctccgctctctctccaca	2040
QY	2041	gtgcgtgctctctctgaggaaactccaaactccctctggtctctcccaaccccgctcccaactc	2100
Db	2041	gtgcgtgctctctctgaggaaactccaaactccctctggtctctcccaaccccgctcccaactc	2100
QY	2101	cccccaactgaaacatgagcaggtctagagctgaaagctccagagctctctctgaaactgag	2160
Db	2101	cccccaactgaaacatgagcaggtctagagctgaaagctccagagctctctctgaaactgag	2160
QY	2161	tcggccccacatatgggaaacctagtaactctctgtcta	2196
Db	2161	tcggccccacatatgggaaacctagtaactctctgtcta	2196

```
: Sequence 1, Application US/09592595
: GENERAL INFORMATION:
: APPLICANT: ROZEN, Rima
: TITLE OF INVENTION: cDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE
: FILE REFERENCE: 04844/005005
: CURRENT APPLICATION NUMBER: US/09/592,595
: CURRENT FILING DATE: 2000-06-12
: PRIOR APPLICATION NUMBER: US 09/258,928
: PRIOR FILING DATE: 1999-03-01
: PRIOR APPLICATION NUMBER: US 08/738,000
: PRIOR FILING DATE: 1997-02-12
: PRIOR APPLICATION NUMBER: PCT/CA95/00314
: PRIOR FILING DATE: 1995-05-25
: PRIOR APPLICATION NUMBER: GB 9410620.0
: PRIOR FILING DATE: 1994-05-26
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 1
: LENGTH: 2220
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(1980)
: US-09-592-595-1
```

```
Query Match          99.6%; Score 2186.6; DB 22; Length 2220;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 1 aatcccgagcgcatggtgagacgaagccagagaaacagacccctcagcttgtag 60
Db 1 aatcccgagcgcatggtgagacgaagccagagaaacagacccctcagcttgtag 60
QY 61 ggcagctgcacacgctgagcagtgagagctccaaagatagttcgagatctccaccccgagc 120
Db 61 ggcagctgcacacgctgagcagtgagagctccaaagatagttcgagatctccaccccgagc 120
QY 121 ctggaacccctgagcgagcatgtagagactccgaggagaagatgagcgagcttgtagtctggt 180
Db 121 ctggaacccctgagcgagcatgtagagactccgaggagaagatgagcgagcttgtagtctggt 180
QY 181 gacacagtggtctccctcggaaattcttcctcctcctcgaactgctgagagagctgtcaatctc 240
Db 181 gacacagtggtctccctcggaaattcttcctcctcctcgaactgctgagagagctgtcaatctc 240
QY 241 atctcaaggtttgacccgagatgagcaggtgagccctctacacagacgtgagctggcac 300
Db 241 atctcaaggtttgacccgagatgagcaggtgagccctctacacagacgtgagctggcac 300
QY 301 ccagcaggtgacccctgctcagacagaagaaactccctccatgatcgcgcagcagcc 360
Db 301 ccagcaggtgacccctgctcagacagaagaaactccctccatgatcgcgcagcagcc 360
QY 361 gtgaactactgtgctcgtgagacacatctcctgacatgacccgtcgcgcctcgtgag 420
Db 361 gtgaactactgtgctcgtgagacacatctcctgacatgacccgtcgcgcctcgtgag 420
QY 421 ggaatacagcgccatctgacacaaagctaagcagctgagcctgaggaacatcatctgctg 480
Db 421 ggaatacagcgccatctgacacaaagctaagcagctgagcctgaggaacatcatctgctg 480
QY 481 cgggagacccaataagtgtagccagtgagagagagagauagagcttcaactcgcagctg 540
Db 481 cgggagacccaataagtgtagccagtgagagagagagauagagcttcaactcgcagctg 540
QY 541 gacctgtgaaagcacaatccgaagttagttgtgactacttgacactctgtgtgagaggt 600
Db 541 gacctgtgaaagcacaatccgaagttagttgtgactacttgacactctgtgtgagaggt 600
QY 601 taacccaagcgcaaccccggaagcagagagctttagagctgacactgaaagcacttgaaagag 660
```

```
Db 601 taacccaagcgcaaccccggaagcagagagctttagagctgacactgaaagcacttgaaagag 660
QY 661 aaggtgtnlcgagagccgattctacatcacagcagcttctcttgagctgacacatc 720
Db 661 aaggtgtnlcgagagccgattctacatcacagcagcttctcttgagctgacacatc 720
QY 721 ttcgcttgtagaagcagtcagccgacatgagcatcaactctcccaatcgctcccgagtc 780
Db 721 ttcgcttgtagaagcagtcagccgacatgagcatcaactctcccaatcgctcccgagtc 780
QY 781 ttcccatcagaagcgtacacactccctcggcagctgtgtaagctgtccaaagttagagtg 840
Db 781 ttcccatcagaagcgtacacactccctcggcagctgtgtaagctgtccaaagttagagtg 840
QY 841 ccacagagatcaagaagcgtgattgagccaatcaaaagacaaagatgtagcatccgcagac 900
Db 841 ccacagagatcaagaagcgtgattgagccaatcaaaagacaaagatgtagcatccgcagac 900
QY 901 tatggcatcagagctgagcgtgagcctgtgacagagagcttctgccaagtggctgtgtgca 960
Db 901 tatggcatcagagctgagcgtgagcctgtgacagagagcttctgccaagtggctgtgtgca 960
QY 961 ggcctcactctacacccctcaaccccgagagatgcttacacagagagtgctgaagcgctg 1020
Db 961 ggcctcactctacacccctcaaccccgagagatgcttacacagagagtgctgaagcgctg 1020
QY 1021 gggatgtgagatgagagaccccaagcgtccctacacctcgtccttaagtgtccacccaag 1080
Db 1021 gggatgtgagatgagagaccccaagcgtccctacacctcgtccttaagtgtccacccaag 1080
QY 1081 cgcagagagagagatgtagctccacatctctcgggctccacagacaaagatgtacatcac 1140
Db 1081 cgcagagagagagatgtagctccacatctctcgggctccacagacaaagatgtacatcac 1140
QY 1141 cgtacccaagagtgtagcagagttccctaaacggcgctgagggaactctctccctcgtgc 1200
Db 1141 cgtacccaagagtgtagcagagttccctaaacggcgctgagggaactctctccctcgtgc 1200
QY 1201 ttgaggagcgtgagagactatacctctctacactcgaagagacaggtccccaagagagag 1260
Db 1201 ttgaggagcgtgagagactatacctctctacactcgaagagacaggtccccaagagagag 1260
QY 1261 ctgctgaagatgtgaggagagagcctgancagtgaaagcaagtgtcttngaagctctgt 1320
Db 1261 ctgctgaagatgtgaggagagagcctgancagtgaaagcaagtgtcttngaagctctgt 1320
QY 1321 cttaactctcggagagaacccaacgggaatgtgtacaaagtgaacttgcctgcctggaac 1380
Db 1321 cttaactctcggagagaacccaacgggaatgtgtgtacaaagtgaacttgcctgcctggaac 1380
QY 1381 gatgagccctctgagctgagacagcctgctgaaagagagagcgtcgcgggtgaaacgcg 1440
Db 1381 gatgagccctctgagctgagacagcctgctgaaagagagagcgtcgcgggtgaaacgcg 1440
QY 1441 caggagcatctctcaacatcaactcaagcccaacatcaacaggggaagccgctcccgaccc 1500
Db 1441 caggagcatctctcaacatcaactcaagcccaacatcaacaggggaagccgctcccgaccc 1500
QY 1501 atcgtgagcgtgagcccaacgggggtatgtcttccagaagagcgtctaaaggttttc 1560
Db 1501 atcgtgagcgtgagcccaacgggggtatgtcttccagaagagcgtctaaaggttttc 1560
QY 1561 acttcccgagagacagcagacactctcgaagtgtctgaagagtagcagctccggtt 1620
Db 1561 acttcccgagagacagcagacactctcgaagtgtctgaagagtagcagctccggtt 1620
QY 1621 aattacacacttgtaagtgtgaaggtgtgaataacatacgaatgcccctgaaactgcagcgg 1680
Db 1621 aattacacacttgtaagtgtgaaggtgtgaataacatacgaatgcccctgaaactgcagcgg 1680
QY 1681 aatgctgtcaactgtgggcatcttccctggcgagagatcatcagccacccgtagtggat 1740
Db 1681 aatgctgtcaactgtgggcatcttccctggcgagagatcatcagccacccgtagtggat 1740
```



Db 1681 aatgctgcatcttgaggcatcttccctggcgagagatcaccagcccaaccgtatgagat 1740  
QY 1741 ccgcgtcaatcattgtctctggaagagagagccttgcctctgtagattgagcgttgagg 1800  
Db 1741 ccgcgtcaatcattgtctctggaagagagagccttgcctctgtagattgagcgttgagg 1800  
QY 1801 aagctgtatgagagagagagccttgcctctgtagattgagcgttgagg 1800  
Db 1801 aagctgtatgagagagagagccttgcctctgtagattgagcgttgagg 1800  
QY 1861 ttccctgtcaacacgtgagacatgacttcccatctgagacacgtcctctgagagtggtg 1920  
Db 1861 ttccctgtcaacacgtgagacatgacttcccatctgagacacgtcctctgagagtggtg 1920  
QY 1921 gaagacacatgagagccttctcaacagcccaacagaaatgagagagagagagagagagag 1980  
Db 1921 gaagacacatgagagccttctcaacagcccaacagaaatgagagagagagagagagagag 1980  
QY 1981 tgacccgtgctgagacagcctgctgtgagagccacatctctcccgcttctctccaca 2040  
Db 1981 tgacccgtgctgagacagcctgctgtgagagccacatctctcccgcttctctccaca 2040  
QY 2041 gtgctgtctctctggaagac 2100  
Db 2041 gtgctgtctctctggaagac 2100  
QY 2101 ccccaactggaacatgagagtagagtagagtagagtagagtagagtagagtagagtagag 2160  
Db 2101 ccccaactggaacatgagagtagagtagagtagagtagagtagagtagagtagagtagag 2160  
QY 2161 tcggcccaacatggaagacatgactctctctctctctctctctctctctctctctct 2196  
Db 2161 tcggcccaacatggaagacatgactctctctctctctctctctctctctctctctct 2196

## RESULT 12

US-09-592-595A-1  
Sequence 1, Application US/09592595A  
GENERAL INFORMATION:  
APPLICANT: ROZEN, Rima  
TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE  
FILE REFERENCE: 04844/005003  
CURRENT APPLICATION NUMBER: US/09/592, 595A  
CURRENT FILING DATE: 2000-06-12  
PRIOR APPLICATION NUMBER: US 09/258, 928  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: US 08/738, 000  
PRIOR FILING DATE: 1997-02-12  
PRIOR APPLICATION NUMBER: PCT/CA95/00314  
PRIOR FILING DATE: 1995-05-25  
PRIOR APPLICATION NUMBER: GB 9410620.0  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 2220  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1980)  
US-09-592-595A-1

Query Match 99.6%; Score 2186.6; DB 22; Length 2220;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 aatccgagacatgtagaagaaacacgagagaaacacacacacacacacacacacacacacac 60  
Db 1 aatccgagacatgtagaagaaacacgagagaaacacacacacacacacacacacacacacac 60

QY 61 ggcagtgccagcagtgagcagtgagagagctccaaagatagctcgaagatgttccaccaccgggc 120  
Db 61 ggcagtgccagcagtgagcagtgagagagctccaaagatagctcgaagatgttccaccaccgggc 120  
QY 121 ctggaccctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 180  
Db 121 ctggaccctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 180  
QY 181 gacaagtggttccctctggaattcttccctcctcgaagctgagagagagagagagagagag 240  
Db 181 gacaagtggttccctctggaattcttccctcctcgaagctgagagagagagagagagagag 240  
QY 241 atctcaaggtttgacccgagatgagcagagtgagcctcctacataagagtgagccttgagac 300  
Db 241 atctcaaggtttgacccgagatgagcagagtgagcctcctacataagagtgagccttgagac 300  
QY 301 ccagcagtgagacccctgctcagacagagagagacacacacacacacacacacacacacac 360  
Db 301 ccagcagtgagacccctgctcagacagagagagacacacacacacacacacacacacacac 360  
QY 361 gtgaactactgtgctctgagagac 420  
Db 361 gtgaactactgtgctctgagagac 420  
QY 421 gagaatacagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480  
Db 421 gagaatacagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480  
QY 481 cggagagac 540  
Db 481 cggagagac 540  
QY 541 gacctgtgagagac 600  
Db 541 gacctgtgagagac 600  
QY 601 taacccaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 660  
Db 601 taacccaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 660  
QY 661 aaggtgtgagagac 720  
Db 661 aaggtgtgagagac 720  
QY 721 ttccgcttgtgagagac 780  
Db 721 ttccgcttgtgagagac 780  
QY 781 ttcccatccagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 840  
Db 781 ttcccatccagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 840  
QY 841 ccaacagagac 900  
Db 841 ccaacagagac 900  
QY 901 tatggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 960  
Db 901 tatggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 960  
QY 961 ggcctcactctac 1020  
Db 961 ggcctcactctac 1020  
QY 1021 gggatgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1080  
Db 1021 gggatgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1080  
QY 1081 cgcagagagagagatgtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1140  
Db 1081 cgcagagagagagatgtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1140  
QY 1141 cgtaccagagagtgagagagagtgccctaaacgagcagcagcagcagcagcagcagcagcagc 1200



```

Db 1141 cgtaccacagatgtagcagatctccctacacgcccgcctgggcaattccctctccctccgc 1200
QY 1201 ttctggagagctggaagcctactactctctctaccttgaaagcgaagctccccaagagag 1260
Db 1201 ttctggagagctggaagcctactactctctctaccttgaaagcgaagctccccaagagag 1260
QY 1261 ctgctgaagatgtaggggagagagctgaaagctgaaagcgaagctgctctgaagctctgct 1320
Db 1261 ctgctgaagatgtaggggagagagctgaaagcgaagctgaaagcgaagctgctctgaag 1320
QY 1321 cttaacctctcgggagagacccaacccggaatgctacaaatgacttgcctgcctggaac 1380
Db 1321 cttaacctctcgggagagacccaacccggaatgctacaaatgacttgcctgcctggaac 1380
QY 1381 gatgaagcccttgccgctgtagacacagcctgtagaagagagagctgctgcgggtgaaccgc 1440
Db 1381 gatgaagcccttgccgctgtagacacagcctgtagaagagagagctgctgcgggtgaaccgc 1440
QY 1441 caaggatctctacatcaatcaatcaacagcccaatcaacagggagccgctctccgacccc 1500
Db 1441 caaggatctctacatcaatcaatcaacagcccaatcaacagggagccgctctccgacccc 1500
QY 1501 atcgtggcctggggccccaacggggtatgctctccagaagagccctactagaagcttttc 1560
Db 1501 atcgtggcctggggccccaacggggtatgctctccagaagagccctactagaagcttttc 1560
QY 1561 acttcccgcgagacagcggagacactctgcaagctgtagaagagtagaagacgctcgggt 1620
Db 1561 acttcccgcgagacagcggagacactctgcaagctgtagaagagtagaagacgctcgggt 1620
QY 1621 aattacacacctgtcatatgtagaggttgaaatacatcaatgccccctgaactgcagccg 1680
Db 1621 aattacacacctgtcatatgtagaggttgaaatacatcaatgccccctgaactgcagccg 1680
QY 1681 aatgctgtcaacttgaggcactctccctgggagagatcatcacaagccacggtagtggat 1740
Db 1681 aatgctgtcaacttgaggcactctccctgggagagatcatcacaagccacggtagtggat 1740
QY 1741 cccgtacagctcatgtcttgagagagcggagccttgcctctgagatgtagcgggtggga 1800
Db 1741 cccgtacagctcatgtcttgagagagcggagccttgcctctgagatgtagcgggtggga 1800
QY 1801 aagctgtatgagagagagagctcccgctccgacacatcatcagtagatccacagcaactac 1860
Db 1801 aagctgtatgagagagagagctcccgctccgacacatcatcagtagatccacagcaactac 1860
QY 1861 aagctgtatgagagagagagctcccgctccgacacatcatcagtagatccacagcaactac 1860
Db 1861 aagctgtatgagagagagagctcccgctccgacacatcatcagtagatccacagcaactac 1860
QY 1861 ttccctgtcaacctgtagaagctgtagaagcttcccaactgtagaagcttccctgtagaag 1920
Db 1861 ttccctgtcaacctgtagaagctgtagaagcttcccaactgtagaagcttccctgtagaag 1920
QY 1921 gaaagacacatgtagaagcttctcaacagccacacagacatgtagaagctgtagaagcttca 1980
Db 1921 gaaagacacatgtagaagcttctcaacagccacacagacatgtagaagctgtagaagcttca 1980
QY 1981 tgaacctgtgctctgtagaagcctgtagaagcctgtagaagcctgtagaagcctgtagaag 2040
Db 1981 tgaacctgtgctctgtagaagcctgtagaagcctgtagaagcctgtagaagcctgtagaag 2040
QY 2041 gtagctgtctctctgtagaagcctgtagaagcctgtagaagcctgtagaagcctgtagaag 2100
Db 2041 gtagctgtctctctgtagaagcctgtagaagcctgtagaagcctgtagaagcctgtagaag 2100
QY 2101 ccccaactgtagaagcctgtagaagcctgtagaagcctgtagaagcctgtagaagcctgtagaag 2160
Db 2101 ccccaactgtagaagcctgtagaagcctgtagaagcctgtagaagcctgtagaagcctgtagaag 2160
QY 2161 tgggccccacatgtagaagcctgtagaagcctgtagaagcctgtagaagcctgtagaagcctgtagaag 2196
Db 2161 tgggccccacatgtagaagcctgtagaagcctgtagaagcctgtagaagcctgtagaagcctgtagaag 2196

```

RESULT 13

```

US-09-660-872-1
; Sequence 1, Application US/09660872
; GENERAL INFORMATION:
; APPLICANT: ROZEN, Rima
; APPLICANT: GOYETTE, Philippe
; TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETETRAHYDROFOLATE
; TITLE OF INVENTION: REDUCTASE
; FILE REFERENCE: 04844/005004
; CURRENT APPLICATION NUMBER: US/09/660,872
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: GB 9410620.0
; PRIOR FILING DATE: 1994-05-26
; PRIOR APPLICATION NUMBER: US 08/738,000
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: US 09/258,928
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1980)
US-09-660-872-1

```

Query Match 99.7%; Score 2186.6; DB 26; Length 2220;

Best Local Similarity 99.7%; Pred. No. 0; Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

QY 1 aattccgagacatgtagaagcgaagccagaggaacagcagcctcaaccctgcttggag 60
Db 1 aattccgagacatgtagaagcgaagccagaggaacagcagcctcaaccctgcttggag 60
QY 61 gggagtgccagcagctgtagaagctcccaagatagtcgaagatgtccaccccgagc 120
Db 61 gggagtgccagcagctgtagaagctcccaagatagtcgaagatgtccaccccgagc 120
QY 121 ctggaacctggaagcagtagaagacatccgggaggaatgtagcggagatgtagaactggt 180
Db 121 ctggaacctggaagcagtagaagacatccgggaggaatgtagcggagatgtagaactggt 180
QY 181 gacaagtgtctccctggaatctctccctcctcgaactgtagaagctgtagaactc 240
Db 181 gacaagtgtctccctggaatctctccctcctcgaactgtagaagctgtagaactc 240
QY 241 atctcaagcttggacggagtagcagaggtggccctctacatagacgtgtagaactgcac 300
Db 241 atctcaagcttggacggagtagcagaggtggccctctacatagacgtgtagaactgcac 300
QY 301 ccagcagtgacacctgtagcacaagaagagacatccctcatatgtagatgcagcagcc 360
Db 301 ccagcagtgacacctgtagcacaagaagagacatccctcatatgtagatgcagcagcc 360
QY 361 gtagaactatgtagcctgtagaagacatctctgtagaagctgtagcctgtagaag 420
Db 361 gtagaactatgtagcctgtagaagacatctctgtagaagctgtagcctgtagaag 420
QY 421 gtagatcacgggcatctgacaaaagctaaagcagctgtagaagcctgtagaagcctgtagaag 480
Db 421 gtagatcacgggcatctgacaaaagctaaagcagctgtagaagcctgtagaagcctgtagaag 480
QY 481 cggggagacccaatagtgtagcagtgaggaaagagagagagagcttcaactaagcagtg 540
Db 481 cggggagacccaatagtgtagcagtgaggaaagagagagagagcttcaactaagcagtg 540
QY 541 gacctgtgtagaagcacatccgaagtagagcttggtagaactcttgacatctgtgtgagag 600
Db 541 gacctgtgtagaagcacatccgaagtagagcttggtagaactcttgacatctgtgtgagag 600
QY 601 taaccacaaggccaccccgaaagcaggagctttagagctgtagaagcacttgaagag 660

```

```
Db 601 taacccaaagccaccccgaaagcgttgaagccgacccgaaagcacttgaaggag 660
Oy 661 aaggtgntgcggagccgattcatcatcacgcagcttctcttgaggctgacacatc 720
Db 661 aaggtgtcgcggagccgattcatcatcacgcagcttctcttgaggctgacacatc 720
Oy 721 ttccgcttctgaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 780
Db 721 ttccgcttctgaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 780
Oy 781 ttcccatccaggccacccaccccttcgacgctgtgaagctgtccagctgaggtg 840
Db 781 ttcccatccaggccacccaccccttcgacgctgtgaagctgtccagctgaggtg 840
Oy 841 ccacagagatcaagagcgtgtatgagccaatcaaaagacagatgctccacgcaac 900
Db 841 ccacagagatcaagagcgtgtatgagccaatcaaaagacagatgctccacgcaac 900
Oy 901 tatgcatcagctgcgctgagcctgtgacagagcttcctgacagtgctggtgcca 960
Db 901 tatgcatcagctgcgctgagcctgtgacagagcttcctgacagtgctggtgcca 960
Oy 961 ggcctcaacttctacacccctcaacccgagatgctacacagaggtgctgaagcgctg 1020
Db 961 ggcctcaacttctacacccctcaacccgagatgctacacagaggtgctgaagcgctg 1020
Oy 1021 gggatgtgactgagagaccccgagcgtccctacacccctgctgctcagtgctccacccaaag 1080
Db 1021 gggatgtgactgagagaccccgagcgtccctacacccctgctgctcagtgctccacccaaag 1080
Oy 1081 cgcgcgagaggaagatgtagctccatctctctgagcctccagaccaaagatatactac 1140
Db 1081 cgcgcgagaggaagatgtagctccatctctctgagcctccagaccaaagatatactac 1140
Oy 1141 cgtacccagagtgaggagagctccctacacccgctgagggaattccctccctgcgc 1200
Db 1141 cgtacccagagtgaggagagctccctacacccgctgagggaattccctccctgcgc 1200
Oy 1201 ttgaggagagtgaaagactactactctctctacctgaagaggaagtcgcccaaggagag 1260
Db 1201 ttgaggagagtgaaagactactactctctctacctgaagaggaagtcgcccaaggagag 1260
Oy 1261 ctgcgtgaagatgtgggggagagagctgagcagtgagcaagtgctcttgaattctgtt 1320
Db 1261 ctgcgtgaagatgtgggggagagagctgagcagtgagcaagtgctcttgaattctgtt 1320
Oy 1321 cttacactctcgggagaaacccaacccggaatggtlcaacaaagtactgtcgtccctggaac 1380
Db 1321 cttacactctcgggagaaacccaacccggaatggtlcaacaaagtactgtcgtccctggaac 1380
Oy 1381 gatgagccctcggcgctgagagccagcctgtctgaagagagagctgtcgggtgaacgc 1440
Db 1381 gatgagccctcggcgctgagagccagcctgtctgaagagagagctgtcgggtgaacgc 1440
Oy 1441 cagggcagcctcctacacatcaactcacagcccaacatcaacgaggaacgctctcccgaccc 1500
Db 1441 cagggcagcctcctacacatcaactcacagcccaacatcaacgaggaacgctctcccgaccc 1500
Oy 1501 atcgtggagctggggcccgagcggtgctatgcttcacagagcctacttagagttttc 1560
Db 1501 atcgtggagctggggcccgagcggtgctatgcttcacagagcctacttagagttttc 1560
Oy 1561 acttcccgagacagcggaagcacttctgcaagtgtcgaagaaatagaagctcgggtt 1620
Db 1561 acttcccgagacagcggaagcacttctgcaagtgtcgaagaaatagaagctcgggtt 1620
Oy 1621 aattacacactgttcaatgtgaaggttgaaaaacatcaccaatgcccctgaaactgacgcg 1680
Db 1621 aattacacactgttcaatgtgaaggttgaaaaacatcaccaatgcccctgaaactgacgcg 1680
Oy 1681 aatgtgtcacttgggagatcttcctcgtgggagagatcacccagccacgtgtgagat 1740
Db 1681 aatgtgtcacttgggagatcttcctcgtgggagagatcacccagccacgtgtgagat 1740
```

```
Db 1681 aatgtgtcacttgggagatcttcctcgtgggagagatcacccagccacgtgtgagat 1740
Oy 1741 ccgcagacttcatgttcttgaaagagacgagccttgccttgtagattgaagcgttgggaa 1800
Db 1741 ccgcagacttcatgttcttgaaagagacgagccttgccttgtagattgaagcgttgggaa 1800
Oy 1801 aagctgtatgagaggaatccccgtcccgacacatcatcacagttacatcacgaactac 1860
Db 1801 aagctgtatgagaggaatccccgtcccgacacatcatcacagttacatcacgaactac 1860
Oy 1861 ttccgtgtaaacctgtgtgaacatgacttccacatgacacactgctcctgtgaggtg 1920
Db 1861 ttccgtgtaaacctgtgtgaacatgacttccacatgacacactgctcctgtgaggtg 1920
Oy 1921 gaagacacattgagagcttctcaacagccacccacgaatgctgagagaaacggaagctcca 1980
Db 1921 gaagacacattgagagcttctcaacagccacccacgaatgctgagagaaacggaagctcca 1980
Oy 1981 tgaccctgctcgtgagcgcctgctgagagcactcctgtccgccttctcctccaca 2040
Db 1981 tgaccctgctcgtgagcgcctgctgagagcactcctgtccgccttctcctccaca 2040
Oy 2041 gtctgtctctcttgaggaaactcactcctcctgtctcctccaccccgctcactc 2100
Db 2041 gtctgtctctcttgaggaaactcactcctcctgtctcctccaccccgctcactc 2100
Oy 2101 cccacacgtgacaaatgagcagctagagtgagagcttccagagcttcttcctgagacag 2160
Db 2101 cccacacgtgacaaatgagcagctagagtgagagcttccagagcttcttcctgagacag 2160
Oy 2161 tcggccacatgaggaaactagtaactctctgctcta 2196
Db 2161 tcggccacatgaggaaactagtaactctctgctcta 2196

RESULT 14
US-09-660-872A-1
; Sequence 1, Application US/09660872A
; GENERAL INFORMATION:
; APPLICANT: ROZEN, Rima
; APPLICANT: GOVETTE, Philippe
; TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE
; TITLE OF INVENTION: REDUCTASE
; FILE REFERENCE: 04844/005004
; CURRENT APPLICATION NUMBER: US/09/660, 872A
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: PCT/IB00/00442
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/258, 928
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: US 08/738, 000
; PRIOR FILING DATE: 1997-02-12
; PRIOR APPLICATION NUMBER: PCT/CA95/00314
; PRIOR FILING DATE: 1995-05-25
; PRIOR APPLICATION NUMBER: GB 9410620.0
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2220
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1980)
; US-09-660-872A-1

Query Match 99.6%; Score 2186.6; DB 26; Length 2220;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Oy 1 aatcggagacatgtgtaacgaagccagaggaacacagcagcctcaacccctgttgag 60
```

Db 1 aattccggaagcgaatgtaacggaagccaagaagccaagccacccctcgtcttgag 60  
 QY 61 ggcagtgcacgaatgagcaatgaaagataagttcgaatgttccacccgggc 120  
 Db 61 ggcagtgcacgaatgagcaatgaaagataagttcgaatgttccacccgggc 120  
 QY 121 ctggaacctgagcgcatagagagactccgggagagagatgagcgagcttgaaatcgt 180  
 Db 121 ctggaacctgagcgcatagagagactccgggagagagatgagcgagcttgaaatcgt 180  
 QY 181 gacaatggtcttcctcctgaaattcttcctcctcgaactcgtgagggagcgtcaatctc 240  
 Db 181 gacaatggtcttcctcctgaaattcttcctcctcgaactcgtgagggagcgtcaatctc 240  
 QY 241 atctcaaggtctgacggagcagcaggtgccccctctcaataagacgtgaaactgac 300  
 Db 241 atctcaaggtctgacggagcagcaggtgccccctctcaataagacgtgaaactgac 300  
 QY 301 ccagcaggtgacacctggtctcagaacaagagacctctcctcaatgatactgcacacccgc 360  
 Db 301 ccagcaggtgacacctggtctcagaacaagagacctctcctcaatgatactgcacacccgc 360  
 QY 361 gtaaacatactgtgacctgagcagacatctctgacatactgacctgcgcctcagcgctgag 420  
 Db 361 gtaaacatactgtgacctgagcagacatctctgacatactgacctgcgcctcagcgctgag 420  
 QY 421 gaagatacgggccaatctgcaacaagaactaagcagctgacctgaggaacatactgacgt 480  
 Db 421 gaagatacgggccaatctgcaacaagaactaagcagctgacctgaggaacatactgacgt 480  
 QY 481 cgggaggaacccaataagtgtaaccagtggaagagagagagagcgttcaactacgcagtg 540  
 Db 481 cgggaggaacccaataagtgtaaccagtggaagagagagagagcgttcaactacgcagtg 540  
 QY 541 gacctgtgaaagacatactccaagtgaagttgtggtgacctacttgacatctgtgtgcaagt 600  
 Db 541 gacctgtgaaagacatactccaagtgaagttgtggtgacctacttgacatctgtgtgcaagt 600  
 QY 601 taacccaagggccaccccggaagcagagactttgagagctgacactgaaagcagctgaaagg 660  
 Db 601 taacccaagggccaccccggaagcagagactttgagagctgacactgaaagcagctgaaagg 660  
 QY 661 aaggtgtmvgcgggagacgaattcatcatcagcagcttctcttgaagctgacacatc 720  
 Db 661 aaggtgtmvgcgggagacgaattcatcatcagcagcttctcttgaagctgacacatc 720  
 QY 721 ttccggttctgtaagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 780  
 Db 721 ttccggttctgtaagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 780  
 QY 781 ttcccatcagggctacacactccctctcgcaagctgtgtaagctgtccaaagctggaggtg 840  
 Db 781 ttcccatcagggctacacactccctctcgcaagctgtgtaagctgtccaaagctggaggtg 840  
 QY 841 ccaacggagatataagagacgtgtatgagccaatacaagaacagatgctgcacatccgcaac 900  
 Db 841 ccaacggagatataagagacgtgtatgagccaatacaagaacagatgctgcacatccgcaac 900  
 QY 901 tatgcatcgaagctgagcgtgagcgtgtgacggagactcttgccaggtgtgtgtgtgtgtgt 960  
 Db 901 tatgcatcgaagctgagcgtgagcgtgtgagcgtgtgagcgtgtgtgtgtgtgtgtgtgt 960  
 QY 961 ggcctccactctacacacctcaacccgagagatgtaaccaagaggtgtgtgtgtgtgtgtgt 1020  
 Db 961 ggcctccactctacacacctcaacccgagagatgtaaccaagaggtgtgtgtgtgtgtgtgt 1020  
 QY 1021 gggatgtgagctgagagaccccgagctcccttaacctgctcgaatgtgtgtgtgtgtgtgt 1080  
 Db 1021 gggatgtgagctgagagaccccgagctcccttaacctgctcgaatgtgtgtgtgtgtgtgt 1080  
 QY 1081 cgcagaggaagatgtaactcctctctgtgacctcaagaacaaaggttatactac 1140  
 Db 1081 cgcagaggaagatgtaactcctctctgtgacctcaagaacaaaggttatactac 1140

Db 1081 cgcagaggaagatgtaactcctctctgtgacctcaagaacaaaggttatactac 1140  
 QY 1141 cgtaccagaggtgtgagcagatctccataacggccgctgtgggcaattctctctccctgc 1200  
 Db 1141 cgtaccagaggtgtgagcagatctccataacggccgctgtgggcaattctctctccctgc 1200  
 QY 1201 ttgtggagagctgaaagactactactctctctcaacctgaaagcagaatcccccaagagagag 1260  
 Db 1201 ttgtggagagctgaaagactactactctctctcaacctgaaagcagaatcccccaagagagag 1260  
 QY 1261 ctgctgaagatgtgtggggagagagctgancagtgaaacaaagtgtctcttgaagatctgtt 1320  
 Db 1261 ctgctgaagatgtgtggggagagagctgancagtgaaacaaagtgtctcttgaagatctgtt 1320  
 QY 1321 cttaactctcgggagagaaaccaacgggaatggttcaacaagtgtactgtcctgtccctgaa 1380  
 Db 1321 cttaactctcgggagagaaaccaacgggaatggttcaacaagtgtactgtcctgtccctgaa 1380  
 QY 1381 gatagacccctgtggtgtgagacagcctgtgaagagagagctgtgcgggtgaaacgc 1440  
 Db 1381 gatagacccctgtggtgtgagacagcctgtgaagagagagctgtgcgggtgaaacgc 1440  
 QY 1441 cagggcactctcaacatacaacccaagccaacatacaacggagagccgtctccgaaccc 1500  
 Db 1441 cagggcactctcaacatacaacccaagccaacatacaacggagagccgtctccgaaccc 1500  
 QY 1501 atcgtggcgtggggccccaaggggtatgctctccaagagcctacttaagatttctc 1560  
 Db 1501 atcgtggcgtggggccccaaggggtatgctctccaagagcctacttaagatttctc 1560  
 QY 1561 acttcccgagagacagcggagacactctctgcaagctgtgaaagagatagagacccgggt 1620  
 Db 1561 acttcccgagagacagcggagacactctctgcaagctgtgaaagagatagagacccgggt 1620  
 QY 1621 aattaccaactgttcaatgtgaaggggtgaaaaatacaaccaatgcccctgaaactgcagcg 1680  
 Db 1621 aattaccaactgttcaatgtgaaggggtgaaaaatacaaccaatgcccctgaaactgcagcg 1680  
 QY 1681 aatgctgtcaactgtgggcatctctccctgtgagagagatactccagcccaacgtaagat 1740  
 Db 1681 aatgctgtcaactgtgggcatctctccctgtgagagagatactccagcccaacgtaagat 1740  
 QY 1741 cccgtcagcttcatgtctctgaaagagcagccttgcgcctgtgaaatgtgagcgtgtggga 1800  
 Db 1741 cccgtcagcttcatgtctctgaaagagcagccttgcgcctgtgaaatgtgagcgtgtggga 1800  
 QY 1801 aagctgtatgagagagagtcgccgtccgcgaacatacatcagatataccaagcaaacatac 1860  
 Db 1801 aagctgtatgagagagagtcgccgtccgcgaacatacatcagatataccaagcaaacatac 1860  
 QY 1861 ttccctgtcaaacctgtgtgaaatgaaattcccaactgaaacactgctctgcaagtgtgtg 1920  
 Db 1861 ttccctgtcaaacctgtgtgaaatgaaattcccaactgaaacactgctctgcaagtgtgtg 1920  
 QY 1921 gaaagacaattgagagcttctcaacaggccaacccaagaatgtgcgagaaacggagagctcca 1980  
 Db 1921 gaaagacaattgagagcttctcaacaggccaacccaagaatgtgcgagaaacggagagctcca 1980  
 QY 1981 tgaacctgctctcagcgcctgtcgltgagccaactctgtgccgctctctctccacaca 2040  
 Db 1981 tgaacctgctctcagcgcctgtcgltgagccaactctgtgccgctctctctccacaca 2040  
 QY 2041 gtgcgtctctctgtgggaactcaactctctctcgtgtctctccaccccggtctcaatc 2100  
 Db 2041 gtgcgtctctctgtgggaactcaactctctctcgtgtctctccaccccggtctcaatc 2100  
 QY 2101 ccccaactgacaatgtgacagctagactgtgaggtcttccagagctctctctgtgacctgag 2160  
 Db 2101 ccccaactgacaatgtgacagctagactgtgaggtcttccagagctctctctgtgacctgag 2160  
 QY 2161 tcggccccacatgtggaacctagactctctgtcta 2196  
 Db 2161 tcggccccacatgtggaacctagactctctgtcta 2196

RESULT 15

IS-09-728-910-1

Sequence 1, Application US/09728910

GENERAL INFORMATION:

APPLICANT: Rozen, Rima

TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE

FILE REFERENCE: 04844/006001

CURRENT APPLICATION NUMBER: US/09/728,910

PRIOR FILING DATE: 2000-12-01

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FASTSD for Windows Version 4.0

SEQ ID NO: 1

LENGTH: 2220

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(1980)

US-09-728-910-1

Query Match 99.6%; Score 2186.6; DB 29; Length 2220;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 aattcggagcattgtgaaacgaagccagaggaacagcagctcacaacccctgctggag 60  
 Db 1 aattcggagcattgtgaaacgaagccagaggaacagcagctcacaacccctgctggag 60  
 QY 61 ggcagctgcagcaatgagcagtgagagctcacaagatagtctgagatgttccaccgggc 120  
 Db 61 ggcagctgcagcaatgagcagtgagagctcacaagatagtctgagatgttccaccgggc 120  
 QY 121 ctgagacctgagcgagcagtgagagagctccgggagagagatgagggcgagattggaatcgtg 180  
 Db 121 ctgagacctgagcgagcagtgagagagctccgggagagagatgagggcgagattggaatcgtg 180  
 QY 181 gacaagtgtcttcctctgaaattcttcctctcgaactgctgagggagctgtcaatctc 240  
 Db 181 gacaagtgtcttcctctgaaattcttcctctcgaactgctgagggagctgtcaatctc 240  
 QY 241 atctcaaggtttgacccgagatgacagcaagtggtccctctacatagacgtgacttgagac 300  
 Db 241 atctcaaggtttgacccgagatgacagcaagtggtccctctacatagacgtgacttgagac 300  
 QY 301 ccagcaggtgacccctgagctcagacagagagacctctccatgatgatcgacagccgc 360  
 Db 301 ccagcaggtgacccctgagctcagacagagagacctctccatgatgatcgacagccgc 360  
 QY 361 gtgaactactgtgacctgagagacatctctgacatgacctctgctgctcagcagctggag 420  
 Db 361 gtgaactactgtgacctgagagacatctctgacatgacctctgctgctcagcagctggag 420  
 QY 421 gggatcacgggcatctgacacaaactaaagcagctgggctgaggaatcaatcagtcgctg 480  
 Db 421 gggatcacgggcatctgacacaaactaaagcagctgggctgaggaatcaatcagtcgctg 480  
 QY 481 cgggagagaccacaatagtgacacagtgagagagagagagagagagagagagagagagag 540  
 Db 481 cgggagagaccacaatagtgacacagtgagagagagagagagagagagagagagagagag 540  
 QY 541 gacctgtgaaagacatccgaagtgagcttgactacttgaaactctgtgtgagag 600  
 Db 541 gacctgtgaaagacatccgaagtgagcttgactacttgaaactctgtgtgagag 600  
 QY 601 taacccaagagccaccggaagcagagagcttgagagctgacctgagacattgagagag 660  
 Db 601 taacccaagagccaccggaagcagagagcttgagagctgacctgagacattgagagag 660

Db 601 taacccaagagccaccggaagcagagagcttgagagctgacctgagacattgagagag 660  
 QY 661 aaggtgtgacggagagcagatctcaatcagcagcttctcttgaaggctgaacattc 720  
 Db 661 aaggtgtgacggagagcagatctcaatcagcagcttctcttgaaggctgaacattc 720  
 QY 721 ttccgcttggaaagcagatcagcagacatgagcagcttgcctccatctgctccggagtc 780  
 Db 721 ttccgcttggaaagcagatcagcagacatgagcagcttgcctccatctgctccggagtc 780  
 QY 781 ttcccatccagggctacacactcccttcgagagcttggagagcttgcctccagagtg 840  
 Db 781 ttcccatccagggctacacactcccttcgagagcttggagagcttgcctccagagtg 840  
 QY 841 ccaacagagatcacaagagcagtgatgagcacaatcaaaagacagatgctgcacatcgcaac 900  
 Db 841 ccaacagagatcacaagagcagtgatgagcacaatcaaaagacagatgctgcacatcgcaac 900  
 QY 901 tatgacatcagctgagcagtgagcagctgtgccaagagcttctgagcagatgagctgggca 960  
 Db 901 tatgacatcagctgagcagtgagcagctgtgccaagagcttctgagcagatgagctgggca 960  
 QY 961 ggcctccatctcacaacccctcaacccgagagatgctacacagagtgctgaagcgctg 1020  
 Db 961 ggcctccatctcacaacccctcaacccgagagatgctacacagagtgctgaagcgctg 1020  
 QY 1021 gggatgtgactgagagacccagcgctccctacactgctgagagagagagagagag 1080  
 Db 1021 gggatgtgactgagagacccagcgctccctacactgctgagagagagagagagag 1080  
 QY 1081 cgcagagagagagatgtgtcgtccatctctcgggctccagacacaagagatcaatcac 1140  
 Db 1081 cgcagagagagagatgtgtcgtccatctctcgggctccagacacaagagatcaatcac 1140  
 QY 1141 cgtacccaagagtgagagcagatgtccctaaacggcgctggggcaattctctccctggc 1200  
 Db 1141 cgtacccaagagtgagagcagatgtccctaaacggcgctggggcaattctctccctggc 1200  
 QY 1201 ttgaggagacagagacatacctctctacactgagagagagagagagagagagag 1260  
 Db 1201 ttgaggagacagagacatacctctctacactgagagagagagagagagagagag 1260  
 QY 1261 ctgctaaagatgtgagggagagagagctgacagtgagagagagagagagagagagag 1320  
 Db 1261 ctgctaaagatgtgagggagagagagctgacagtgagagagagagagagagagagag 1320  
 QY 1321 cttactctctcgggagaaacacacacggagatgtgacaaagtgactgctgctcgagac 1380  
 Db 1321 cttactctctcgggagaaacacacacggagatgtgacaaagtgactgctgctcgagac 1380  
 QY 1381 gatgagccctctgagcagtgagacacagctgagagagagagagagagagagagag 1440  
 Db 1381 gatgagccctctgagcagtgagacacagctgagagagagagagagagagagagag 1440  
 QY 1441 cagggcatctctacacatcaacatcagcccaacatacaacggagagagagagagagag 1500  
 Db 1441 cagggcatctctacacatcaacatcagcccaacatacaacggagagagagagagagag 1500  
 QY 1501 atcgtgagcagggccacacgggggctatgctctcagaagagcctactaagagatttcc 1560  
 Db 1501 atcgtgagcagggccacacgggggctatgctctcagaagagcctactaagagatttcc 1560  
 QY 1561 acttcggcagagacagcagagacattctgcaagtgctgagagagagagagagagagag 1620  
 Db 1561 acttcggcagagacagcagagacattctgcaagtgctgagagagagagagagagagag 1620  
 QY 1621 aattacacacctgtgcaatgtgaaagtgaaacacacacacacacacacacacacacac 1680  
 Db 1621 aattacacacctgtgcaatgtgaaagtgaaacacacacacacacacacacacacacac 1680  
 QY 1681 aatgtgacttgaggagatctccctggcgagagagatccatccagggccacagagagag 1740  
 Db 1681 aatgtgacttgaggagatctccctggcgagagagatccatccagggccacagagagag 1740

```
QY 1741 ccgcgcagcttcattcttgaaagacagagccttgcctgtagattgagcggtggga 1800
    |||||||
Db 1741 ccgcgcagcttcattcttgaaagacagagccttgcctgtagattgagcggtggga 1800
    |||||||
QY 1801 aagctgtagagagagagtcctccgctccgcacatccagtagatccacgacaactac 1860
    |||||||
Db 1801 aagctgtagagagagagtcctccgctccgcacatccagtagatccacgacaactac 1860
    |||||||
QY 1861 ttctctgtagaacctggtgagacaatgacttcccaactggaactgctctgcaagtggtg 1920
    |||||||
Db 1861 ttctctgtagaacctggtgagacaatgacttcccaactggaactgctctgcaagtggtg 1920
    |||||||
QY 1921 gaagacacattgagagcttcccaacagcccaacagaaatgcgagagaacgagagctcca 1980
    |||||||
Db 1921 gaagacacattgagagcttcccaacagcccaacagaaatgcgagagaacgagagctcca 1980
    |||||||
QY 1981 tgacctgagctcctgacgacctgctgtagagccactcctgtcccgcttctcctccaca 2040
    |||||||
Db 1981 tgacctgagctcctgacgacctgctgtagagccactcctgtcccgcttctcctccaca 2040
    |||||||
QY 2041 gtgctgcttctcttggaactccacttctctgtgtctctccaccccgctcnaactc 2100
    |||||||
Db 2041 gtgctgcttctcttggaactccacttctctgtgtctctccaccccgctcnaactc 2100
    |||||||
QY 2101 cccacactgacaatgagcagtagactgagtgagagcttccagctcttctctggaactgag 2160
    |||||||
Db 2101 cccacactgacaatgagcagtagactgagtgagagcttccagctcttctctggaactgag 2160
    |||||||
QY 2161 tcggccccacatgaggaaactagtaactctctctcta 2196
    |||||||
Db 2161 tcggccccacatgaggaaactagtaactctctctcta 2196
    |||||||
```

Search completed: June 26, 2002, 18:37:35  
Job time: 10587 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 26, 2002, 16:20:18 ; Search time 321.18 Seconds  
(Without alignments)  
10443.366 Million cell updates/sec

Title: **SEQ1MOD**  
Perfect score: 2196  
Sequence: 1 aatccgagcagcatgttgaa.....acctaagtactctgtctcta 2196

Scoring table:  
IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1044500 seqs, 763706786 residues  
Total number of hits satisfying chosen parameters: 2089000

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : Pending\_Patents\_NA\_New:\*  
1: /cgn2\_6/pdata/1/pna/PCT\_NEW\_COMB.seq:\*  
2: /cgn2\_6/pdata/1/pna/US06\_NEW\_COMB.seq:\*  
3: /cgn2\_6/pdata/1/pna/US07\_NEW\_COMB.seq:\*  
4: /cgn2\_6/pdata/1/pna/US08\_NEW\_COMB.seq:\*  
5: /cgn2\_6/pdata/1/pna/US09\_NEW\_COMB.seq:\*  
6: /cgn2\_6/pdata/1/pna/US10\_NEW\_COMB.seq:\*  
7: /cgn2\_6/pdata/1/pna/US10\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2188	99.6	2196	US-09-638-267-1	Sequence 1, Appl
2	2186.6	99.6	2219	US-09-931-795-3	Sequence 3, Appl
3	2186.6	99.6	2220	US-09-931-795-1	Sequence 1, Appl
4	2177.6	99.2	2187	US-09-371-347A-51	Sequence 51, Appl
5	305.2	13.9	1689	US-60-360-039-27188	Sequence 27188, A
6	237.8	10.8	1994	PCT-US02-10064-3	Sequence 3, Appl
7	194	8.8	1800	US-60-360-039-45612	Sequence 45612, A
8	194	8.8	3082	PCT-US02-10064-1	Sequence 1, Appl
9	184.6	8.4	1809	US-60-360-039-25804	Sequence 25804, A
10	110.6	5.0	112	PCT-US01-47593-21	Sequence 21, Appl
11	110.6	5.0	112	PCT-US01-47593-23	Sequence 23, Appl
12	77.6	3.5	323	US-09-975-254-15156	Sequence 25, Appl
13	64.8	3.0	2031	US-60-360-039-26809	Sequence 26809, A
14	62.4	2.8	1923	US-09-975-254-20206	Sequence 20206, A
15	61.6	2.8	353	US-60-360-039-29215	Sequence 29215, A
16	50	2.3	1974	US-60-360-039-46191	Sequence 46191, A
17	49.4	2.2	1974	US-60-360-039-46191	Sequence 46191, A
18	49	2.2	50	US-09-940-244-214	Sequence 214, App
19	48.2	2.2	2187	US-09-371-347A-51	Sequence 51, Appl
20	48.2	2.2	2219	US-09-931-795-3	Sequence 3, Appl
21	48.2	2.2	2220	US-09-931-795-1	Sequence 1, Appl
22	47.8	2.2	1089	US-09-540-2098-4276	Sequence 4276, App
23	47.8	2.2	2196	US-09-638-267-1	Sequence 1, Appl
24	47.4	2.2	50	US-09-940-244-215	Sequence 215, App
25	46	2.1	28882	US-10-158-844-140	Sequence 140, App
26	44.8	2.0	271	US-09-975-254-24417	Sequence 24417, A

27	44.4	2.0	278	5	US-09-540-2108-33036	Sequence 33036, A
28	43.6	2.0	1275	7	US-60-360-039-32228	Sequence 32228, A
29	43	2.0	376	7	US-60-360-039-43150	Sequence 43150, A
30	42.6	1.9	295	5	US-09-442-366A-303	Sequence 303, App
31	42	1.9	63	1	PCT-US01-47593-24	Sequence 24, Appl
32	41.6	1.9	249	5	US-09-975-254-24386	Sequence 24386, A
33	40.8	1.9	245	5	US-09-975-254-19625	Sequence 19625, A
34	40.6	1.8	833	6	US-10-143-775-116	Sequence 116, App
35	40.6	1.8	1743	7	US-60-360-039-43111	Sequence 43111, A
36	40.4	1.8	63	1	PCT-US01-47593-25	Sequence 25, Appl
37	40.4	1.8	200	5	US-09-540-2108-11178	Sequence 11178, A
38	40.4	1.8	3036	5	US-09-053-3758-1472	Sequence 1472, App
39	40.4	1.8	3036	5	US-09-442-384B-471	Sequence 471, App
40	39.8	1.8	1182	7	US-60-360-039-24247	Sequence 24247, A
41	39.8	1.8	5877	6	US-10-152-886-54	Sequence 54, Appl
42	39.6	1.8	1329	7	US-60-360-039-31633	Sequence 31633, A
43	39.4	1.8	594	6	US-10-123-155-10	Sequence 10, Appl
44	39.4	1.8	594	6	US-10-137-871-10	Sequence 10, Appl
45	39.4	1.8	594	6	US-10-141-761-10	Sequence 10, Appl

## ALIGNMENTS

```

RESULT 1
US-09-638-267-1
; Sequence 1, Application US/09638267
; GENERAL INFORMATION:
; APPLICANT: Stanton, Jr., Vincent P.
; TITLE OF INVENTION: GENE SEQUENCE VARIANCES IN GENES RELATED
; TITLE OF INVENTION: TO FOLATE METABOLISM HAVING UTILITY IN
; FILE REFERENCE: 11926-092001
; CURRENT APPLICATION NUMBER: US/09/638,267
; CURRENT FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 09/596,033
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 09/357,743
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 09/357,024
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: 60/093,484
; PRIOR FILING DATE: 1998-07-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: misc-feature
; LOCATION: 1784
; FEATURE:
; OTHER INFORMATION: n = a or g
; NAME/KEY: misc-feature
; LOCATION: 464
; FEATURE:
; OTHER INFORMATION: n = g or t
; NAME/KEY: misc-feature
; LOCATION: 1289
; FEATURE:
; OTHER INFORMATION: n = c or a
; US-09-638-267-1

```

Query Match 99.6%; Score 2188; DB 5; Length 2196;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2191; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 aattccgagcattggtgaacgaagccaaggaacagcctcaaccctgtctgag 60  
Db 1 aattccgagcattggtgaacgaagccaaggaacagcctcaaccctgtctgag 60  
QY 61 ggcagctgccaagctggcagctgagagctccaagaatagttcgaagatgttccaccgagc 120  
Db 61 ggcagctgccaagctggcagctgagagctccaagaatagttcgaagatgttccaccgagc 120  
QY 121 ctggaacctgagcggcattgagagctcccgagagaaatgagcgagctggaaatctggt 180  
Db 121 ctggaacctgagcggcattgagagctcccgagagaaatgagcgagctggaaatctggt 180  
QY 181 gacaaagtggtctccctggaaattctccctcctcgaactgtctgagggagcgtcaatctc 240  
Db 181 gacaaagtggtctccctggaaattctccctcctcgaactgtctgagggagcgtcaatctc 240  
QY 241 atctcaaggtttgacggatgagcagctgagccctctacataagacgtgaactggac 300  
Db 241 atctcaaggtttgacggatgagcagctgagccctctacataagacgtgaactggac 300  
QY 301 ccagcagaagtacccctggctcagagaagaagcctccctcagatgattcgccagacagcc 360  
Db 301 ccagcagaagtacccctggctcagagaagaagcctccctcagatgattcgccagacagcc 360  
QY 361 gtgaaactactgtgctcgtgagagacatcctgacatagacctgtgcgtcagcgctgag 420  
Db 361 gtgaaactactgtgctcgtgagagacatcctgacatagacctgtgcgtcagcgctgag 420  
QY 421 gagatcacgggcacatctgcacaagaagctaagcagctggcctgagagaacatactgcgt 480  
Db 421 gagatcacgggcacatctgcacaagaagctaagcagctggcctgagagaacatactgcgt 480  
QY 481 cggagagaaccaataggtgacccagctggagaagagaaugagagcttcaatacagagtg 540  
Db 481 cggagagaaccaataggtgacccagctggagaagagaaugagagcttcaatacagagtg 540  
QY 541 gacctgtgaaagcacatcccgaaagttagtctgtaactactttgacatctgtgtgagcag 600  
Db 541 gacctgtgaaagcacatcccgaaagttagtctgtaactactttgacatctgtgtgagcag 600  
QY 601 taacccaaaaggcccccgcgaagcagggagctttgagctgcacccgaagcacttgaagag 660  
Db 601 taacccaaaaggcccccgcgaagcagggagctttgagctgcacccgaagcacttgaagag 660  
QY 661 aaggtgtgtgagcagcagattcatcatcacgagctttctcttggagctgcacattc 720  
Db 661 aaggtgtgtgagcagcagattcatcatcacgagctttctcttggagctgcacattc 720  
QY 721 ttccgctttgtgaaagcattgcacggacatgagcatcaacttgcgccatcgtcccgagtc 780  
Db 721 ttccgctttgtgaaagcattgcacggacatgagcatcaacttgcgccatcgtcccgagtc 780  
QY 781 ttcccaatcgaaggctacacactcccttcggaagcttggaaagctgtccaagctggaagt 840  
Db 781 ttcccaatcgaaggctacacactcccttcggaagcttggaaagctgtccaagctggaagt 840  
QY 841 ccacaaagagatcaaggaagctgattgagccaatcaaaagacaagatgctgcacatccgaac 900  
Db 841 ccacaaagagatcaaggaagctgattgagccaatcaaaagacaagatgctgcacatccgaac 900  
QY 901 tatggatctgagctggcgtgagagctgtgcacgaagcttctgccaagtgtgtgtcca 960  
Db 901 tatggatctgagctggcgtgagagctgtgcacgaagcttctgccaagtgtgtgtcca 960  
QY 961 ggcctcaactctacacccctcaaacgcgagatggtctacacagaggtgtgaagcgctgt 1020  
Db 961 ggcctcaactctacacccctcaaacgcgagatggtctacacagaggtgtgaagcgctgt 1020  
QY 1021 gggagtgtgagctgagagccccaagcgtccctacacctgcgctctcaatgtgccacccaag 1080  
Db 1021 gggagtgtgagctgagagccccaagcgtccctacacctgcgctctcaatgtgccacccaag 1080

QY 1081 cgcgagagagaaatgtacgtcccatctctgggcctccagaccacaagagttaacatctac 1140  
Db 1081 cgcgagagagaaatgtacgtcccatctctgggcctccagaccacaagagttaacatctac 1140  
QY 1141 cgtaccagaagctgtgagcagagttccctcaacggcgcgtgaggcaattccctctccctgc 1200  
Db 1141 cgtaccagaagctgtgagcagagttccctcaacggcgcgtgaggcaattccctctccctgc 1200  
QY 1201 ttgttgagagctggaagagctactacattctctacatctggaagaaagagctccccaagagag 1260  
Db 1201 ttgttgagagctggaagagctactacattctctacatctggaagaaagagctccccaagagag 1260  
QY 1261 ctgctgaagatgtgtgggagagctgancagtgaaacaaagtgtcttngaagctctgtt 1320  
Db 1261 ctgctgaagatgtgtgggagagctgancagtgaaacaaagtgtcttngaagctctgtt 1320  
QY 1321 cttaacctctcggagaaaccaacccggaatgttcaaaagtgaactgtcgtccctggaac 1380  
Db 1321 cttaacctctcggagaaaccaacccggaatgttcaaaagtgaactgtcgtccctggaac 1380  
QY 1381 gatgagccctgtgcgtggaagacagcctgtgaaaggagagagctgtcgggtgaacgc 1440  
Db 1381 gatgagccctgtgcgtggaagacagcctgtgaaaggagagagctgtcgggtgaacgc 1440  
QY 1441 cagggcatacctcaacatcaactcaacagccacaatcaacaggaagcgtctcccgaaacc 1500  
Db 1441 cagggcatacctcaacatcaactcaacagccacaatcaacaggaagcgtctcccgaaacc 1500  
QY 1501 atcgtgtgctgtgggcccagcggggtctatgtcttccagaagagcctactaagatttctc 1560  
Db 1501 atcgtgtgctgtgggcccagcggggtctatgtcttccagaagagcctactaagatttctc 1560  
QY 1561 acttcccgcgagacagcggaagcacttctcgaagtgtgaaagagctacggagctccgggt 1620  
Db 1561 acttcccgcgagacagcggaagcacttctcgaagtgtgaaagagctacggagctccgggt 1620  
QY 1621 aattaccaactctgtcaaatgtgaaaggtgaaacacacccaatgtcccttgaaatgcagcg 1680  
Db 1621 aattaccaactctgtcaaatgtgaaaggtgaaacacacccaatgtcccttgaaatgcagcg 1680  
QY 1681 aatgtctgaactgtgggcatcttccctggggtggaagatcatccagcccaacgtagtgat 1740  
Db 1681 aatgtctgaactgtgggcatcttccctggggtggaagatcatccagcccaacgtagtgat 1740  
QY 1741 cccgtcagctcatgcttctgaaagcagagccttgcctgtgagatctgagcgttggga 1800  
Db 1741 cccgtcagctcatgcttctgaaagcagagccttgcctgtgagatctgagcgttggga 1800  
QY 1801 aagctgtatgagagaggtcccgctcccgacacatcatcaagtaacatccacgaacatcac 1860  
Db 1801 aagctgtatgagagaggtcccgctcccgacacatcatcaagtaacatccacgaacatcac 1860  
QY 1861 ttccctgtcaaacctgtgtgaaatgaattcccaatggaacactgtcctgtgaggtgtgt 1920  
Db 1861 ttccctgtcaaacctgtgtgaaatgaattcccaatggaacactgtcctgtgaggtgtgt 1920  
QY 1921 gaaagacacatttgagcttctcaaacagcccaacccaagaaatgcgaagaaagagagcttca 1980  
Db 1921 gaaagacacatttgagcttctcaaacagcccaacccaagaaatgcgaagaaagagagcttca 1980  
QY 1981 tgaccctgtcctctgagacgcctgtgtgagccaactctgttcccgcttctctccaca 2040  
Db 1981 tgaccctgtcctctgagacgcctgtgtgagccaactctgttcccgcttctctccaca 2040  
QY 2041 gtgtgtcttctcctgtggaacacacactcctctctgtgctctcccaaccccggtctcaatc 2100  
Db 2041 gtgtgtcttctcctgtggaacacacactcctctctgtgctctcccaaccccggtctcaatc 2100  
QY 2101 ccccaacctgacaatgtgagctagatctgaggttcccaagcctctctctgtgaacctggag 2160  
Db 2101 ccccaacctgacaatgtgagctagatctgaggttcccaagcctctctctgtgaacctggag 2160  
QY 2161 tcggccccaatggaacctagatctctctgtctcta 2196





Db 1561 attcccgagagacaggaagcattctgcaagtgctgaagaaglacagctccgggtc 1620  
QY 1621 aattaccactgtcatgtgaagggtgaaatacatcccaatccctgactgacggcg 1680  
Db 1621 aattaccactgtcatgtgaagggtgaaatacatcccaatccctgactgacggcg 1680  
QY 1681 aatgtctcatcttgggcatctctccctggcgagagatacatccagccacagctagtgat 1740  
Db 1681 aatgtctcatcttgggcatctctccctggcgagagatacatccagccacagctagtgat 1740  
QY 1741 cccgttaagcttcatgtcttggaagagagagccttggcctgtagattgagcggtggga 1800  
Db 1741 cccgttaagcttcatgtcttggaagagagagccttggcctgtagattgagcggtggga 1800  
QY 1801 aagcttatgagagagatccccgcgcgcacatcatccagtafacatccacagcaactac 1860  
Db 1801 aagcttatgagagagatccccgcgcgcacatcatccagtafacatccacagcaactac 1860  
QY 1861 ttccgtgtaaacctgtgtgaaatagaacttcccaatggaactgtccttggcaggtggtg 1920  
Db 1861 ttccgtgtaaacctgtgtgaaatagaacttcccaatggaactgtccttggcaggtggtg 1920  
QY 1921 gaagacaacttgagacttctccaaacagccacagaaatgcgaagaagagaggtccca 1980  
Db 1921 gaagacaacttgagacttctccaaacagccacagaaatgcgaagaagagaggtccca 1980  
QY 1981 tgaacctgctctgaacgcgcctgcttggagccaactctgttccgccttctctccaca 2040  
Db 1981 tgaacctgctctgaacgcgcctgcttggagccaactctgttccgccttctctccaca 2040  
QY 2041 ggtgtctctcttcttggaactcactctcttctgttcttccacacccggctccactc 2100  
Db 2041 ggtgtctctcttcttggaactcactctcttctgttcttccacacccggctccactc 2100  
QY 2101 ccccaactgacaatgagcagctagactgagtgaggttccaggtcttccctgagactgag 2160  
Db 2101 ccccaactgacaatgagcagctagactgagtgaggttccaggtcttccctgagactgag 2160  
QY 2161 tcggcccaatgaggaactagtaactctctgctcta 2196  
Db 2161 tcggcccaatgaggaactagtaactctctgctcta 2196

RESULT 3  
US-09-931-795-1  
Sequence 1, Application US/09931795  
GENERAL INFORMATION:  
APPLICANT: ROZEN, Rama  
TITLE OF INVENTION: CDNA FOR HUMAN METHYLENETHETRAHYDROFOLATE  
TITLE OF INVENTION: REDUCTASE AND USES THEREOF  
FILE REFERENCE: 04844/005003  
CURRENT APPLICATION NUMBER: US/09/931,795  
PRIOR FILING DATE: 2001-08-16  
PRIOR APPLICATION NUMBER: US 09/592,595  
PRIOR FILING DATE: 2000-06-12  
PRIOR APPLICATION NUMBER: US 09/258,928  
PRIOR FILING DATE: 1999-03-01  
PRIOR APPLICATION NUMBER: US 08/738,000  
PRIOR FILING DATE: 1997-02-12  
PRIOR APPLICATION NUMBER: PCT/CA95/00314  
PRIOR FILING DATE: 1995-05-25  
PRIOR APPLICATION NUMBER: GB 9410620.0  
PRIOR FILING DATE: 1994-05-26  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 2220  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(1980)  
US-09-931-795-1

Query Match 99.6%; Score 2186.6; DB 5; Length 2220;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2189; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 aattccggaacccaatggtgaacgaagccagaggaacagcagcctcaaacccctgcttgag 60  
Db 1 aattccggaacccaatggtgaacgaagccagaggaacagcagcctcaaacccctgcttgag 60  
QY 61 ggcagtgccagcagtgagcagtgagagctccaaagatagtcagatgttccacccgggc 120  
Db 61 ggcagtgccagcagtgagcagtgagagctccaaagatagtcagatgttccacccgggc 120  
QY 121 ctggaacctgaagagatagagaaactccgggaagaataggggagattggaatttgtt 180  
Db 121 ctggaacctgaagagatagagaaactccgggaagaataggggagattggaatttgtt 180  
QY 181 gacaagtggttctccctggaattcttccctcctcgaactgtgagggagctgtcaatttc 240  
Db 181 gacaagtggttctccctggaattcttccctcctcgaactgtgagggagctgtcaatttc 240  
QY 241 atctcaaggtttgacccgagatgagcagagtgagccctcctcaataagacgtgagctggcac 300  
Db 241 atctcaaggtttgacccgagatgagcagagtgagccctcctcaataagacgtgagctggcac 300  
QY 301 ccagcaggtgagacctgtgctcaagacaaagagacctcctccaatgatactgcacacagccgc 360  
Db 301 ccagcaggtgagacctgtgctcaagacaaagagacctcctccaatgatactgcacacagccgc 360  
QY 361 gttgaactactgtgtgctgtgagacacatcctcgcacataagactgtgcctgacgcctggag 420  
Db 361 gttgaactactgtgtgctgtgagacacatcctcgcacataagactgtgcctgacgcctggag 420  
QY 421 gagaatacgggacatctgacaaagctaaagcagcttggccttgaggaacatcatgagcgctg 480  
Db 421 gagaatacgggacatctgacaaagctaaagcagcttggccttgaggaacatcatgagcgctg 480  
QY 481 cgggaggaacccaataggtgacacagtgaggaagaggaagaggtcttaactaactagcagtg 540  
Db 481 cgggaggaacccaataggtgacacagtgaggaagaggaagaggtcttaactaactagcagtg 540  
QY 541 gacctgtgaaagacatccgaagtgaattgtgtgactactttgacatcctgtgtgcaagt 600  
Db 541 gacctgtgaaagacatccgaagtgaattgtgtgactactttgacatcctgtgtgcaagt 600  
QY 601 taaccacaagggccaccccgaaagcagagcttggagcgtgacactgaaagcaacttgaaggag 660  
Db 601 taaccacaagggccaccccgaaagcagagcttggagcgtgacactgaaagcaacttgaaggag 660  
QY 661 aaggtgtntgcgggagcgaattcatcatcaacgacagcttctcttgagcgtgacacatc 720  
Db 661 aaggtgtntgcgggagcgaattcatcatcaacgacagcttctcttgagcgtgacacatc 720  
QY 721 ttccgtttgtgaaagcagacacacagacatgggagatcaacttggcccatgttcccgagatc 780  
Db 721 ttccgtttgtgaaagcagacacacagacatgggagatcaacttggcccatgttcccgagatc 780  
QY 781 ttcccatcgaaggtacacacatccctcctgcgacgtgtgaaagctgtccaaagcttgaggtg 840  
Db 781 ttcccatcgaaggtacacacatccctcctgcgacgtgtgaaagctgtccaaagcttgaggtg 840  
QY 841 ccacagagatacgaagacgtgattgagccaatcaaaagacacagatgtgcatccgcaac 900  
Db 841 ccacagagatacgaagacgtgattgagccaatcaaaagacacagatgtgcatccgcaac 900  
QY 901 tatgagatcagagctggcgttgagcctgtgcaaggagcttctgccaagtgtgctgtgca 960  
Db 901 tatgagatcagagctggcgttgagcctgtgcaaggagcttctgccaagtgtgctgtgca 960  
QY 961 ggcctcaacttaacacccctcaacccgagatgctgataccacagaggtgtctgaaagcctg 1020  
Db 961 ggcctcaacttaacacccctcaacccgagatgctgataccacagaggtgtctgaaagcctg 1020

QY 1021 gggatgtgactgagaccacccagcgctccctacccctgctctcagtcgcccaccccaag 1080  
 |||||  
 Db 1021 gggatgtgactgagaccacccagcgctccctacccctgctctcagtcgcccaccccaag 1080  
 QY 1081 cgcgagagagaaatgtaagtcacgtccatctctcggcctccagacaaagagttacatctac 1140  
 |||||  
 Db 1081 cgcgagagagaaatgtaagtcacgtccatctctcggcctccagacaaagagttacatctac 1140  
 QY 1141 cgtacccagagatgaggag 1200  
 |||||  
 Db 1141 cgtacccagagatgaggag 1200  
 QY 1201 ttctggagagctggaagagactacactctcttaccctggaagagagagagagagagagag 1260  
 |||||  
 Db 1201 ttctggagagctggaagagactacactctcttaccctggaagagagagagagagagagag 1260  
 QY 1261 ctgctgaagatgtgg 1320  
 |||||  
 Db 1261 ctgctgaagatgtgg 1320  
 QY 1321 cttacactcccgagagaaacaaacccggaatggtcacaaagtgaactgtgctgcccctggagc 1380  
 |||||  
 Db 1321 cttacactcccgagagaaacaaacccggaatggtcacaaagtgaactgtgctgcccctggagc 1380  
 QY 1381 gatgagcccttgctgctgagacacagctctggaagagagagagagagagagagagagagc 1440  
 |||||  
 Db 1381 gatgagcccttgctgctgagacacagctctggaagagagagagagagagagagagagagc 1440  
 QY 1441 caggagcactccac 1500  
 |||||  
 Db 1441 caggagcactccac 1500  
 QY 1501 atcgtgggctgg 1560  
 |||||  
 Db 1501 atcgtgggctgg 1560  
 QY 1561 actcccgagagacag 1620  
 |||||  
 Db 1561 actcccgagagacag 1620  
 QY 1621 aattacacactgttcaatgtgaaggggtgaacacacacacacacacacacacacacacacac 1680  
 |||||  
 Db 1621 aattacacactgttcaatgtgaaggggtgaacacacacacacacacacacacacacacacac 1680  
 QY 1681 aatgcttcaacttgaggagacatctccctgggagagagagagagagagagagagagagag 1740  
 |||||  
 Db 1681 aatgcttcaacttgaggagacatctccctgggagagagagagagagagagagagagagag 1740  
 QY 1741 cccgtcagcttcaatgttctggaagagagagagagagagagagagagagagagagagagag 1800  
 |||||  
 Db 1741 cccgtcagcttcaatgttctggaagagagagagagagagagagagagagagagagagagag 1800  
 QY 1801 aagctgtatgag 1860  
 |||||  
 Db 1801 aagctgtatgag 1860  
 QY 1861 ttctctgttcaacactggtggaacatgacttcccatgtggaacatgctcccttggaaggtgtg 1920  
 |||||  
 Db 1861 ttctctgttcaacactggtggaacatgacttcccatgtggaacatgctcccttggaaggtgtg 1920  
 QY 1921 gaagacacatgtgagcttctcaacagagccacacagaaatgagagaaacgagagctca 1980  
 |||||  
 Db 1921 gaagacacatgtgagcttctcaacagagccacacagaaatgagagaaacgagagctca 1980  
 QY 1981 tgaccctggcttctgag 2040  
 |||||  
 Db 1981 tgaccctggcttctgag 2040  
 QY 2041 gtgtgtgtcttctgtggaacacacactctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2100  
 |||||  
 Db 2041 gtgtgtgtcttctgtggaacacacactctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 2100

QY 2101 cccacactgacaaatgagagactagactgagagtgagagcttccaggctcttctgagctgag 2160  
 |||||  
 Db 2101 cccacactgacaaatgagagactagactgagagtgagagcttccaggctcttctgagctgag 2160  
 QY 2161 tcggccccacatgagagactagactctctgtctca 2196  
 |||||  
 Db 2161 tcggccccacatgagagactagactctctgtctca 2196

# RESULT 4

US-09-371-347A-51

; Sequence 51, Application US/09371347A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gravel, Roy A,  
 ; APPLICANT: Rozen, Rima  
 ; APPLICANT: Leclerc, Daniel  
 ; APPLICANT: Wilson, Aaron  
 ; APPLICANT: Rosenblatt, David  
 ; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE REDUCTASE:  
 ; CLONING, AND METHODS FOR EVALUATING RISK OF NEURAL TUBE  
 ; TITLE OF INVENTION: DEFECTS, CARDIOVASCULAR DISEASE, AND CANCER  
 ; FILE REFERENCE: 50004/003003  
 ; CURRENT APPLICATION NUMBER: US/09/371, 347A  
 ; CURRENT FILING DATE: 1999-08-10  
 ; PRIOR FILING DATE: 1999-01-15  
 ; PRIOR APPLICATION NUMBER: 60/071, 622  
 ; PRIOR FILING DATE: 1998-01-16  
 ; NUMBER OF SEQ ID NOS: 61  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 51  
 ; LENGTH: 2187  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-371-347A-51

Query Match 99.2%; Score 2177.6; DB 5; Length 2187;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 2180; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 10 gccatgtgacgaagcag 69  
 |||||  
 Db 1 gccatgtgacgaagcag 60  
 QY 70 agcagtgagtgag 129  
 |||||  
 Db 61 agcagtgagtgag 120  
 QY 130 gagcagatgag 189  
 |||||  
 Db 121 gagcagatgag 180  
 QY 190 ttctcccttggaattcttccctctcctcagagctgagagagagagagagagagagagagag 249  
 |||||  
 Db 181 ttctcccttggaattcttccctctcctcagagctgagagagagagagagagagagagagag 240  
 QY 250 ttgacccgagtgag 309  
 |||||  
 Db 241 ttgacccgagtgag 300  
 QY 310 gaccctggtcag 369  
 |||||  
 Db 301 gaccctggtcag 360  
 QY 370 tgttgagtgag 429  
 |||||  
 Db 361 tgttgagtgag 420  
 QY 430 ggcacatgtgacaaagatgaagcagctggtggtcgtgagagagagagagagagagagagag 489  
 |||||  
 Db 421 ggcacatgtgacaaagatgaagcagctggtggtcgtgagagagagagagagagagagagag 480











OTHER INFORMATION: DNA construct  
PCT-US02-10064-1

Query Match 8.8%; Score 194; DB 1; Length 3082;  
Best Local Similarity 48.7%; Pred. No. 7.6e-36;  
Matches 854; Conservative 0; Mismatches 823; Indels 78; Gaps 9;

```

OY 175 tctgtgcaagtggttcctccgtgaattcttcctccctcgagctgctgaggagctgac 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 865 tctgcaagccacttacttacttacttacttacttacttacttacttacttacttactt 924
OY 235 aatcattcacaaggtttgacccgagatg---gacgaaggtgccccctctacataagctg 291
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 925 aacctgtagcagcgatgacccgagatgtagcaggtcttcttcccaatttattgacac 984
OY 292 acctggcccccgacaggtgagccctgctgacgaagagacctctccctctgattgtcgcc 351
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 985 acctggaatgacggcggtgagcgtttgtcacatctg-----tccaggaacttgctt 1035
OY 352 agcacccgctgaaactactgtgcttgagacacatctgacatgacatctgctgcgtcag 411
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1036 ggcagacggcgacgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1095
OY 412 cgctcgagagagatacagggccatctgacaaagctaaagcagctggtgctgaggaacac 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1096 cccattctgattgacgacgctttagaaacgcttactactccggttgcagagaacac 1155
OY 472 atcgcgctcgaggagacccaataggtgac-----agtggaagagagagagagagc 525
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1156 cttagcgctgagagagatctctctctagggagcagaaactgtgactccgcttgaagtg 1215
OY 526 tccaactacgacgtgacctgtgtgaagacatcccgagctgagctgtgtgactactttgac 585
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1216 ttcggatagcacaagacttctgattagtaataagcttcaagcttaccgcttaccatttgc 1275
OY 586 atctgtgtgagaggttaacccaagaccccgacgaagcagggagcttgaagctgacgcg 645
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1276 atcggcgctgacggctaccccgagtgctcccggaagtgtccctcaacaaagcgtgaag 1335
OY 646 aagcaactgaaagagagtgatgctg---ggaagccgatttcaatcacacgacgtttcc 702
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1336 gatctcgaaattctgacgaagagatcgacggcgagcttactacacacgacgtttt 1395
OY 703 ttgagagctgacacatctctccgcttctgtgaagcactgacacgacacgttgacattgc 762
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1396 taagatgttgaataattacttacttacttacttacttacttacttacttacttactt 1455
OY 763 cccatcgctcccgagatcttcccatccagggcgtaccactcccttcgagcgttgtgaag 822
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1456 cccattatcccgagatctatgctgacatctacacacgacgcttcttgaagaagatccaa 1515
OY 823 cgtgccaagctggaaggtgacacagagatcaagagctgattgagccaatcaagaagacac 882
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1516 tgggggccaatctccatccctcaacattctctgctccgattgtgactatcaagaagcgt 1575
OY 883 gatctgccaatccgcaactatgacacagcgtgacgctgagcgtgtgacagagcgttctg 942
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1576 gacgagttgtccgtgatatcgaaactatgactgtgaaatggtgcaaaaatgtgtc 1635
OY 943 gccagtggtgtgtgacagggcctccacttcaacacacacacacacacacacacacacac 1002
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1636 gacagtggttgaagtttcttacttacttacttacttacttacttacttacttactt 1695
OY 1003 gagggtgctaaagcgcctggggat-----gtggactgagagccacag 1044
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1696 atgattctggaagatgtaaatcttacttacttacttacttacttacttacttacttactt 1755
OY 1045 cgtccctacactgctgctcagtgccaccccaagcgccgagagagagatgtaagctccc 1104
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1756 gccgtgtgctgacatggaagaatcttgaatccaaagcgttaaaacgaggaagtcagact 1815
OY 1105 atcttctggcctccagacaaagttacatctacacacacagagtg-----gac 1158

```

```

DB 1816 atcttctggaagagagacacttacttacttacttacttacttacttacttacttactt 1875
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1159 gattccccaagcgcgcgtggggccaatctctctccctcgtcttgggagctggaagac 1218
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1876 gaattcccaagcgcgcgtggggccaatctctctccctcgtcttgggagcttggagact 1932
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1219 tactacttcttacttacttacttacttacttacttacttacttacttacttacttactt 1278
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1933 ctgtgtgtgctgacttacttacttacttacttacttacttacttacttacttacttactt 1992
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1279 gaggagcgtgaagagagagagagagagagagagagagagagagagagagagagag 1338
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1993 cctacttccatcaagagcgtcgtctcttctgacac----- 2028
OY 1339 ccaaacccggaatgctcacaaagtgaacttgcctgcctcctggaacgagacccctgcgcgt 1398
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2029 ---aactacttgaatggaagacttgaagtgattacttcttggagtgatatacccatgaatgat 2085
OY 1399 gaggacagcctgtgaagagagagagagagagagagagagagagagagagagagagag 1458
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2086 gaataaataatccaatcaagcacacttgaacttgaacttgaacttgaacttgaacttga 2145
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1459 aactcaacgccaacacacacacacacacacacacacacacacacacacacacacacac 1518
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2146 aacttcaacacacacacacacacacacacacacacacacacacacacacacacacacac 2205
OY 1519 agcgggggctatgcttctccagaagccttacttgaagtttctacttcccgagagacagc 1578
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2206 aaggaatggttacttacttacttacttacttacttacttacttacttacttacttactt 2265
OY 1579 gaagcaacttctgcaagtggttgaagagagagagagagagagagagagagagagagag 1638
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2266 cccaagtgtatgtgacacacttgaacaaacatgagcttctgacacttgcctcgaactct 2325
OY 1639 gtgaaggtgtaaaacacacacacacacacacacacacacacacacacacacacacacac 1698
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2326 caagtgacactgtaagtaatcatccacacacacacacacacacacacacacacacacac 2385
OY 1699 atcttcccgcgagagagatctccacacacacacacacacacacacacacacacacacac 1758
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2386 atcttcccgcgagagagatctccacacacacacacacacacacacacacacacacacac 2445
OY 1759 tggaaagcagagccttctccctgtgagatgagcgtgtggggaagcgtgagagagagag 1818
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2446 tggaaagagagagatctccacacacacacacacacacacacacacacacacacacacac 2505
OY 1819 tcccgctccgcacac---atcatcagatcacacacacacacacacacacacacacacac 1875
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2506 aaaccgcatagtgcccaattcattcagcttctgattgacgatatcgtgtgacatatt 2565
OY 1876 gtggacatgacttc 1890
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2566 gtggacatgacttac 2580
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 9  
US-60-360-039-25804  
; Sequence 25804, Application US/60360039

GENERAL INFORMATION:

APPLICANT: Cao, Yongmei

APPLICANT: Chen, Xianfeng

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

FILE REFERENCE: 38-10(52052)A

CURRENT APPLICATION NUMBER: US/60/360,039

CURRENT FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 25804

LENGTH: 1809



RESULT 11  
PCT-US01-47593-23/C  
; Sequence 23, Application PC/TUS0147593  
; GENERAL INFORMATION:  
; APPLICANT: DISCOVERX  
; TITLE OF INVENTION: STRAND DISPLACEMENT DETECTION OF TARGET NUCLEIC ACID  
; FILE REFERENCE: 3817.01-1PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/47593  
; PRIOR FILING DATE: 2001-12-07  
; PRIOR APPLICATION NUMBER: 60/256,737  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 112  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA  
PCT-US01-47593-23

Query Match 5.0%; Score 110.6; DB 1; Length 112;  
Best Local Similarity 98.2%; Pred. No. 1.5e-16;  
Matches 110; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 638 ctgacctgaacactggaaggaaggtgtntgcggagacacattcatcaacagc 697  
|||  
DB 112 CTGACCTGAACACTGGAAGGAGAGGTGTCTCGCGAGCTGATTCATCATCAGCAGC 53  
OY 698 ttctcttgaagctgacacattcttcgcgttctgtgaaggcatgcagcacat 749  
|||  
DB 52 TTTCTTGAAGCTGACACATCTTCCTGTTGTGAAGCATGACCGACAT 1

RESULT 12  
US-09-975-254-15156  
; Sequence 15156, Application US/09975254  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: Heck, Gregory R.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(15309)B  
; CURRENT APPLICATION NUMBER: US/09/975,254  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US/09/263,191  
; PRIOR FILING DATE: 1999-03-05  
; NUMBER OF SEQ ID NOS: 31255  
; SEQ ID NO 15156  
; LENGTH: 323  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: 700862959H1  
US-09-975-254-15156

Query Match 3.5%; Score 77.6; DB 5; Length 323;  
Best Local Similarity 61.0%; Pred. No. 9.4e-09;  
Matches 125; Conservative 0; Mismatches 80; Indels 0; Gaps 0;  
OY 1686 tctcacttgggacattccctcctggcgagagatcatccagccacgtagtgaatccgt 1745  
|||  
DB 1 tctgacatgggggtctctccacgtaagagataatcaaccaacattgtagtctgt 60  
OY 1746 cacttcatgttcggaagcagagccttgcctctgaattgaagcggtgggaagc 1805  
|||  
DB 61 cacttcaatgtatggaagatgagcattgtaattgttcaagagagatgggaagc 120  
OY 1806 gtatgagagagatcccgctcccgacatcatccagtaacatccagcactcttcc 1865  
|||

DB 121 gtacccctgagatgagcattccaggaattgttgaagaagttggggcagccacttct 180  
OY 1866 gtccaactgtgtgacatgactc 1890  
|||  
DB 181 ggtagttgtgcagcaatgattac 205

RESULT 13  
US-60-360-039-26809  
; Sequence 26809, Application US/60360039  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Chen, Xianfeng  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)A  
; CURRENT APPLICATION NUMBER: US/60/360,039  
; CURRENT FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 26809  
; LENGTH: 2031  
; TYPE: DNA  
; ORGANISM: Neurospora crassa  
US-60-360-039-26809

Query Match 3.0%; Score 64.8; DB 7; Length 2031;  
Best Local Similarity 54.7%; Pred. No. 1.2e-05;  
Matches 151; Conservative 0; Mismatches 122; Indels 3; Gaps 1;

OY 1645 ggtgaacatcaccgaatgcccctgaactgcagccgaatgctgtacttgggacattc 1704  
|||  
DB 1759 gctgagccgacacagagccgcattgactgacacacgcgttaacttgggctgttc 1818  
OY 1705 cctggcgagagatcatccagccacgtagtgaatcccgtagtattcttcggaag 1764  
|||  
DB 1819 cccggcaaggaatctcgaagccacatcatcgaggaagtcagcttcgcgctgagc 1878  
OY 1765 gacgagccttgcctctgattgagcggttgggaagctgtatgagagagtcctccg 1824  
|||  
DB 1879 gagagggcttggatttggagcga---gtggccaagatctacggaagagatccgac 1935  
OY 1825 toccgacacatcatcattcaatccacgacaactactcttcgttgaacttgggacat 1884  
|||  
DB 1936 acccagaagttgttggaggaattggaagagatcttgcgtgtgtaattgattcat 1995  
OY 1885 gacttcccatggaacactgcctctggcaggtgtg 1920  
|||  
DB 1996 gattatcttgaagaagcagccttggaaagtgttg 2031

RESULT 14  
US-60-360-039-25852  
; Sequence 25852, Application US/60360039  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Chen, Xianfeng  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)A  
; CURRENT APPLICATION NUMBER: US/60/360,039  
; CURRENT FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 25852  
; LENGTH: 1923  
; TYPE: DNA  
; ORGANISM: Schizosaccharomyces pombe





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 26, 2002, 14:29:33 ; Search time 2329.2 Seconds  
(Without alignments)  
12725.104 Million cell updates/sec

Title: SEQMOD  
Perfect score: 2196  
Sequence: 1 aattcggagcgcattgtgaa.....acttagtactctctgctcta 2196

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estlun:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_estl:\*  
10: gb\_estl2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vit:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	781	35.6	900	10	BG675748
2	542.2	24.7	556	10	BM310814
3	485.8	22.1	563	9	AU129663
4	466.8	21.3	654	9	BB617073
5	458.6	20.9	507	9	AI262190
6	446.4	20.3	556	10	BG384323
7	439.6	20.0	925	10	BI430422
8	434.4	19.8	774	9	AU169401
9	433.8	19.8	537	9	AM050775
10	358	16.3	457	10	BF654483
11	354.4	16.1	398	10	BF930775
12	352.4	16.0	400	10	BF934146
13	332	15.1	549	10	BM089718
14	321.8	14.7	499	9	AA183742
15	320.6	14.6	550	10	BE753120
16	311.4	14.2	650	10	BJ097085
17	309.4	14.1	614	10	BJ070955

18	308.2	14.0	572	9	AL647166
19	305.4	13.9	582	10	BJ069591
20	299.8	13.7	587	9	BE131889
21	295.2	13.4	560	10	BI066086
22	294.4	13.4	580	10	AJ393018
23	292.4	13.3	512	10	BM494723
24	281.8	12.8	335	9	AM436969
25	276.2	12.6	523	10	BJ066114
26	276	12.5	557	10	BJ033632
27	275	12.5	336	9	AM658667
28	273.6	12.5	461	10	BG979786
29	267.8	12.2	336	10	BE706718
30	266	12.1	309	9	AM636737
31	265.4	12.1	286	9	AA340811
32	262	11.9	488	9	BE190101
33	247.4	11.3	450	9	AM645737
34	224.6	10.2	469	10	BI849423
35	223.8	10.2	269	9	AM484848
36	219.8	10.0	223	10	BE244583
37	211.2	9.6	472	10	BG835531
38	209	9.5	437	9	BB850869
39	197.2	9.0	666	10	BJ100073
40	184.4	8.4	249	9	AM478874
41	165.4	7.5	587	10	BJ125503
42	162.8	7.4	986	10	BG745802
43	160.6	7.3	603	9	AU204758
44	160.6	7.2	615	10	BJ108206
45	155.4	7.1	411	9	AU241885

## ALIGNMENTS

RESULT 1  
LOCUS BG675748 900 bp mRNA linear EST 01-MAY-2001  
DEFINITION 602621974F1 NCI\_CGAP\_Skn4 Homo sapiens cDNA clone IMAGE:4746955 5', mRNA sequence.

ACCESSION BG675748  
VERSION BG675748.1 GI:13907144  
KEYWORDS EST.

## ORGANISM

Homo sapiens Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 900)  
NHI-MGC http://mgc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgaps-remail.nih.gov

Tissue Procurement: James Cleaver, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM10596 row: c column: 20  
High quality sequence stop: 894.  
Location/Qualifiers  
1. 900

## FEATURES

source

/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4746955"  
/clone\_1lb="NCI\_CGAP\_Skn4"  
/tissue\_type="squamous cell carcinoma"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.5kb. Library constructed by Life Technologies. Note: This is a NCI\_CGAP Library."  
BASE COUNT 198 a 269 c 247 g 186 t

## ORIGIN

Query Match 35.6%; Score 781; DB 10; Length 900;  
 Best Local Similarity 96.1%; Pred. No. 9.2e-161;  
 Matches 799; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

OY 1234 ctgaagaagcaagtcctcccaagaagagagctgctgaagatgtgggggagagagctgancagt 1293  
 Db 37 CCGCTGACCAAGTCCCGCCCAAGAGAGAGCTGCTGAAGATGTGGGGGAGAGAGCTGACAGT 96  
 OY 1294 gaagaagatgctcctgnaagttcttcttaactctctcggagagaaacaaacgggaatgt 1353  
 Db 97 GAGAGAAATGCTTTGAAAGCTTTGCTTTTACCTTCGGAGAAACCAACCGGAATGCT 156  
 OY 1354 cacaagatgacttgctcctcctggaacatgagccctctgggcttgagaccagctgtctg 1413  
 Db 157 CACAAGAGACTTGCCTGCCCTGGAAGATGAGCCCTGGGCTTGAGACCAAGCTGCTG 216  
 OY 1414 aaggaagagctgctgctggggtggaacccgaagggaatcctcaactcaactcagcccaac 1473  
 Db 217 AAGGAGAGAGCTGCTGCGGGTGAACCGGAGGATCCTCCTCAGCACTCAGAGCCCAAC 276  
 OY 1474 atcaacgggaagccgtctcctcgaacccatgctggtgctggtggcccgagggtatgtc 1533  
 Db 277 ATCAACGGGAAGCGCTCCTCGAACCCATGCTGAGCTGGGCTGGGCGCCAGCGGCTATGTC 336  
 OY 1534 ttccagaagagcttaactagaatttctcaactcccgagagacagcggaagcaactctgcaa 1593  
 Db 337 TTCAGAAAGCGCTTACCTTACCTTCCCGGAGACAGCGGAGAGCACTTCTGCA 396  
 OY 1594 gtgctgaagaagtaagagctccgggttaattacacactgtcaatgtgaaggtgaagac 1653  
 Db 397 GTGCTGAAGAAGTACAGAGCTCCGGGTTAATTACCACTTGTCAATGTGAAGGTGAAAC 456  
 OY 1654 atcaacatgccccctgaactgacgcgaatgtctgtaacttgaggacatctccctgggca 1713  
 Db 457 ATACCAATGCCCCCTGAACCTGACGCGAATGCTGACTTGGGCGCATCTTCCCTGGGCA 516  
 OY 1714 gaagatcacagcccaacgctgaatgagatcccgctcaacttcaatgttctgaagaagagagcc 1773  
 Db 517 GAATATATCAGCCCAACCGCTAGAGTCCCGTACGCTTATGTTCTGGAAGAGCAGGCG 576  
 OY 1774 ttgcccctgtagatgtagagcggtgggaaagcgtatgtagaagagatcccccgcagacc 1833  
 Db 577 TTTGCCCTGTGATTGAGCGGTGGGAAAGCTGATGAGAGAGAGTCCCGTCCGACAC 636  
 OY 1834 atcatccagtaataccaagaacaactactctctgtcaaccttggtgagaaatgaactcca 1893  
 Db 637 ATATCATCATATCATCCAGACAAATTACTCTGCTCAACCTGTGAGACATGACTTCCA 696  
 OY 1894 ctggaacaactgctctgtgcaagtggtggaagaacacatgtggagcttctcaacagcccaac 1953  
 Db 697 CTGGAACAATGCTCTGGCAGAGTGTGGAAGACATTTGGAGCTTCTCAACAGGCGAAC 756  
 OY 1954 cagaaatgagagaaacggaaggtctcatgaccctgctcctgagcgccttgcttggagcc 2013  
 Db 757 CAGAAATGCGAAGAAAGGAGGCTCCATGACCTGCTGCTGACGCCCTGGCTTGGAGCC 816  
 OY 2014 actcctgcccgcctctcctcctcaacagtgcttctctctgggaactcca 2064  
 Db 817 ACTCTGTCTCCCGCTTCTCTCTCACAGTGTCTCTCTCTTGGGAACTCCA 867

RESULT 2  
 BM310814 556 bp mRNA linear EST 03-JAN-2002  
 LOCUS 1948109.v1 HR85 islet Homo sapiens cDNA 5' similar to SW:WTHR\_HUMAN  
 DEFINITION P42898 METHYLENETERAHYDROFOLATE REDUCTASE ;, mRNA sequence.  
 ACCESSION BM310814  
 VERSION BM310814.1 GI:18045159  
 KEYWORDS EST.  
 SOURCE human.

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

## REFERENCE

1 (bases 1 to 556)  
 Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,  
 Lemishka, I., Sceane, M., Brestelli, J., Gradwohl, G., Clifton, S.,  
 Hillier, L., Maira, M., Page, D., Wylie, T., Martin, J., Blistein, A.,  
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas,  
 M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R., Williams, T.,  
 Jackson, Y., and Bowers, Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)  
 Other-ESTs: 1948109.x1

## TITLE

Endocrine Pancreas Consortium  
 Unpublished (2000)  
 Other-ESTs: 1948109.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557

Email: dmelton@biolmp.harvard.edu  
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Dr. Hiroshi Inoue  
 (hinoue@im.wustl.edu)  
 Seq primer: -40RP from Glibco

High quality sequence stop: 429.

## FEATURES

## source

Location/Qualifiers  
 1..556  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="HR85 islet"  
 /tissue\_type="Purified pancreatic islet"  
 /lab\_host="DH10B"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:  
 NotI; Site\_2: XhoI; cDNA made by oligo-dT priming.  
 Size-selected on agarose gel. Average insert size -1kb. 5'  
 XhoI site was destroyed after directional cloning.  
 Amplified once. Contact Information: Hiroshi Inoue, MD,  
 Metabolism Div. (Alan Permut Lab), Washington University  
 School of Medicine, Box 8127, 660 South Euclid Ave., St.  
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:  
 314-362-1916, Fax: 314-747-2692."

BASE COUNT 134 a 156 c 173 g 93 t

## ORIGIN

Query Match 24.7%; Score 542.2; DB 10; Length 556;  
 Best Local Similarity 99.5%; Pred. No. 1.7e-108;  
 Matches 544; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 9 agccatgtgaacgaagccagaggaacagcagcctcaacccctgttggaggagcagtc 68  
 Db 10 AGCCATGTGAACGAAACAGAGAAACAGACCCCTCAACCCCTGCTTGGAGGCAATGC 69  
 OY 69 cagcagtgagcagtgagagctcccaagaatagtcgagatgtccacccgggctgagacc 128  
 Db 70 CAGCAGTGCGAGTGAAGAGCTCCAAAGATGTTGGAATTTCCACCCCGGCTTGAGACC 129  
 OY 129 tgaggagcagtagaagactccgggagagaatgagcgcgagattggaatctggtgacaagt 188  
 Db 130 CGAGCGGCAATGAGAGACTCCGGAGAAAGATGAGCGCGCATTTGGAATCTGGACAACTG 189  
 OY 189 gtctccctggaattctccctcccgaaactgtagagagctgcatcatcattcaag 248  
 Db 190 GTTCTCCCTGGAATTTCTCCCTCGAACTCTAGAGGAGCTGTCAATTCATCTCAAG 249  
 OY 249 gtttagcagatgagcagcagatgtgccccctacatagacgttgacctggcaccagcag 308  
 Db 250 GTTTAGCGGATGCGAGGAGGTGGCCCTCTACATAGACGAGACGTGGCACCGAGAGG 309  
 OY 309 tgaccctgctcagcagagagactcctcatgatgatgtcgccagaccgctgaaacta 368



```

Db      310 TGACCTGCTCAGACAAAGAGACCTCCCTCCATGATGATCGCAGACACCCGCTGAACTA 369
QY      369 ctgtgacctggaagaccatctctgcacatgacctgtgcgttagagcgctggagagatcac 428
Db      370 CTGTGGCTGTGAGACACATCTCTGCACATGACCTGCTGCGTAGAGCGCTGGAGAGATCAC 429
QY      429 gggccatctgcacaaagctaagcagctggcgcttgaggaacatcatctgagcgctggagga 488
Db      430 GGGCATCTGCACAAAGCTAAGCAGCTGGCGCTGAAGAACATCATGGCGCTGGCGGAGGA 489
QY      489 cccaatagtgagaccagtgagggaaggaaggaagagagcttaactacagcagtgagcttgt 548
Db      490 CCCAATAGGTGACCAAGTGGAAGAGAGAGAGAGAGGCTTCACATCACTGACGTGACCTGT 549
QY      549 gaagcac 555
Db      550 GAAACAC 556

RESULT 3
LOCUS   AUI29663
DEFINITION AUI29663 NT2RP2 Homo sapiens cDNA clone NT2RP2005995 5', mRNA
ACCESSION AUI29663
VERSION   AUI29663.1 GI:10990017
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 563)
AUTHORS   Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
           Yamamoto,J., Wakatsuki,A., Nakamura,Y., Nagai,T., Sugano,S. and
           Isogai,T.
TITLE      HRI human cDNA project
JOURNAL   Unpublished (2000)
COMMENT   Contact: Takao Isogai
           Genomics Laboratory
           Helix Research Institute
           1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
           Tel: 81-438-52-3951
           Fax: 81-438-52-3952
           Email: genomics@hri.co.jp
           HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
           Research Institute; cDNA library construction; Department of
           Virology, Institute of Medical Science, University of Tokyo, and
           Helix Research Institute.
FEATURES
  source          1..563
                  location/Qualifiers
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /clone="NT2RP2005995"
                  /clone_1lb="NT2RP2"
                  /cell_type="teratocarcinoma"
                  /cell_line="NT2"
                  /note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
                  cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT      130 a 160 c 175 g 95 t
ORIGIN
Query Match 22.1%; Score 485.8; DB 9; Length 563;
Best Local Similarity 98.8%; Pred. No. 3.8e-96;
Matches 498; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

```

```

QY      129 tgaaggagatgagagagcctcgaggagaagatgagcgcgagattggnatctgtgacaagt 188
Db      181 CGAGCGCATGAGAGACTCCGGAGAGAGATGAGCGCGGATTTGGAAATGTGTGACAAATG 240
QY      189 gtctccctggaaattcttcctcctcctgcgaactgctgaaggagctgcaatctcatcacaag 248
Db      241 GTTCCCTGGAAATCTTCCCTCCCGAAGCTGTGAGGAGACTGTCAATCTCATCTCAAG 300
QY      249 gttgaccggaatgagcagaggttgccccctccttaactaagaagtgagctggcaccagcagg 308
Db      301 GTTTGACCCGATGTGACAGAGGTGGCCCCCTCTACATTAACGTGACCTGGACCCAGCAGG 360
QY      309 tgaccctggtcagacagaagagagacctctcctcatatgtagtcgcaagcagcgctgaacta 368
Db      361 TGACCTGTGCTCAGACAAAGAGACCTCTCCATGATGATCGCACACCGCGGTGAACCTA 420
QY      369 ctgtgacctgagagaccatctgcacatgacctgtgcctgcagcgacctgagagagatcac 428
Db      421 CTGTGGCTGTGAGACACATCTCTGCACATGACCTGCTGCCGCTGAGGAGAGATCAC 480
QY      429 gggccatctgcacaaagctaagcagctggcgcttgaggaacatcatgctgagggagaga 488
Db      481 GGGCATCTGCACAAAGCTAAGCAGCTGGCGCTGAANAAACATCATGCGCTGGCGGAGANA 540
QY      489 cccaatagtgagcagctggagaga 512
Db      541 -CCAATAGGTGACCAAGTGGAANA 563

RESULT 4
LOCUS   BB617073
DEFINITION BB617073 RIKEN full-length enriched, adult male testis Mus musculus
ACCESSION BB617073
VERSION   BB617073.1 GI:15396258
KEYWORDS  EST.
SOURCE    house mouse.
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE 1 (bases 1 to 654)
AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
           Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
           M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Sasaki
           Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
           Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
           Muramatsu,M. and Hayashizaki,Y.
           RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
           Unpublished (2001)
           Contact: Yoshihide Hayashizaki
           Laboratory for Genome Exploration Research Group, RIKEN Genomic
           Sciences Center(GSC), Yokohama Institute
           The Institute of Physical and Chemical Research (RIKEN)
           1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
           Tel: 81-45-503-9222
           Fax: 81-45-503-9216
           Email: genome-res@sc.riken.go.jp,
           URL:http://genome.gsc.riken.go.jp/
           Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
           M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
           Normalization and subtraction of cap-trapper-selected cDNAs to
           prepare full-length cDNA libraries for rapid discovery of new
           genes. Genome Res. 10 (10), 1617-1630 (2000)
           wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
           Wataniki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura
           S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and
           Hayashizaki,Y.
           RIKEN integrated sequence analysis (RISA) system--384-format
           sequencing pipeline with 384 multicapillary sequencer. Genome Res.
           10 (11), 1757-1771 (2000)

```



```

|||||
Db 507 TGGGCACTTCTCCCTGGGGAAGAGATCATCAAGCCACCGTAGTGATCCCGTCAGCTTC 448
Oy 1753 atgtcttggaaggagagagccttgcctgtgatgtgagcgttgaggaaactgtatgag 1812
Db 447 ATGTTCTGGAAGAGAGAGAGCCCTTTCCTGTTGATGAGCGGTGGGAAAGCTGTATGAG 388
Oy 1813 gagaagtcacccgtcccgacacatcaccc-agtaccatccagcagaactacttctt-gtaca 1870
Db 387 NAGGAGTCCCGCTCCCGACCATCATCATCAAGTACATCAAGACCAACTACTTCTTGAGTCA 328
Oy 1871 accgtgtggaacaatgaacttcccaactggaacaactgcctctgagagtggtggaagacacat 1930
Db 327 ACCTGTGGACATGACTTCCCTCAGTGAACACTGACCTCTGGAGGTGGGAAAGACAT 268
Oy 1931 tgaagcttctcaacagagccacccagaatgagagagaagagagctccatgaacctgtg 1990
Db 267 TGGACCTTCTCAACAGAGCCACCCAGAAATGCGAGAGAAAGAGAGCTCCATACCTTGCG 208
Oy 1991 tcttgacgcctctgcttggaagcactcctgtccgccttctcctccacagtgctgttc 2050
Db 207 TCTTACGCCCTTGCGTGGAGCACTCCTGTCGCCGCTTCCTCCACAGTGTGCTTC 148
Oy 2051 tcttggaagcctccactcctcctgtgtctctcccaacccgcctccactccccactgaa 2110
Db 147 TCTTGGAGACTCCACTCTCTGCTGCTCCACCCCGGCTCCACTCCGCCACCTGA 88
Oy 2111 caatggcagctagactgtagtgaagcttccagagcttctccttggaacttgaagtgcccccac 2170
Db 87 CAATGGCAGCTAGACTGAGAGTGAAGCTTCAGAGCTTCTCTGAGACTGAGTGGGCCAC 28
Oy 2171 atgggaacctagactctctgtcctta 2196
Db 27 ATGGGAACCTAGTACTCTGCTCTA 2

RESULT 6
Bg384323 556 bp mRNA linear EST 12-MAR-2001
LOCUS 303363 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.
DEFINITION Bg384323
ACCESSION Bg384323.1 GI:13308795
VERSION EST
KEYWORDS
SOURCE EST
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
REFERENCE 1 (bases 1 to 556)
AUTHORS Fahrenkrug,S.C., Preking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGATCAGCAGC
Plate: 90 row: O column: 22
Seq primer: ATTTAGTGACACTATAG.
FEATURES
source
1. 556
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1Pig"

```

```

/tissue_type="pooled"
/lab_host="DH10B"
/notes="Vector: PCMV SPOR6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 119 a 170 c 162 g 105 t
ORIGIN
Query Match 20.3%; Score 446.4; DB 10; Length 556;
Best Local Similarity 88.7%; Pred. No. 1.7e-87;
Matches 494; Conservative 0; Mismatches 62; Indels 1; Gaps 1;

Oy 427 acgggacatctgcacaaagtaagcagctggcgctgaggaacatcatgctgtgggga 486
Db 1 ACGGCTTACTCTCAACAGGCCCAAGCGCGTGGGCTGA -AAACATCTTGGCGCTGAGGGGA 59
Oy 487 gaccacatagtgaccagtgaggagagagagagagcttcaactacgacgtgacctg 546
Db 60 GACCTGTAGTGTGACACGAGGGAAGAGAGAGAGAGGCTTCAGCTACCTGCAGACTTG 119
Oy 547 gtgaagcacatccgaagtgtgtgtgactacttgcacatctgtgtgcaagttacccc 606
Db 120 GTGAAGCACATCCGACGAGGAGTTGGTACTACTTCAGACGTGTGTGCGCAGGTAACCC 179
Oy 607 aaagggcaccggcgaagcagagagcttggagctgacactgaacacttgaagagaagtg 666
Db 180 AAAGGCAACCCCGACGACAGAGAGCTTGGAGCGGACCTGAACCTGAAGAGAAAGGTG 239
Oy 667 tntgggagccgatttcatacatcagcagcttcttcttgagagctgacacatcttccgc 726
Db 240 GCGGAGAGAGCGGAGCTTATCATCAACCCAGCTTTCTTGAGAGCGTATACGTTCTCCGC 299
Oy 727 ttgtgaaagcgtgacgcagacatgagcacttgcacatctgcctcccgagcttccc 786
Db 300 TTCTTGAAGGCTTGTCTCCGAGATGGGACATCACCTGCCCATCTCCGCGCATCTTCCCC 359
Oy 787 atccagagctaccactcctccttgcagagcttggaaagctgttcaaaactggaagtgcaca 846
Db 360 ATCCAGGGCTTACCTACTCCCTCCGAGCGCTGGAAGCTGTCCAACTGAGAGTGGCCGAG 419
Oy 847 gagatcaagaagcgtgatttgaagcacaatcaaaagacagatgtgcacatccgaactatgac 906
Db 420 CAGATCAAGAGAGCTGTGAGAGGCCCAAGACATGAGCGCGCATCCGCACTATATGGC 479
Oy 907 atcagagctggcgtgagcctgtgccaagagcttctgtgcagtgctgtgtgcagagctc 966
Db 480 ATCGAGCAGGCTGTGAGCTTGTGCGCAGAGCTTGTGCGCAGTGGCTGTGCGCGGCTTC 539
Oy 967 cacttctacacacctcaa 983
Db 540 CACTTCTATACCTCTCA 556

RESULT 7
B1430422 925 bp mRNA linear EST 16-AUG-2001
LOCUS B1430422
DEFINITION UMR39B07 Canine Brain cDNA Library Canis familiaris cDNA 5' similar
to Human 5',10 methyltetrahydrofolate reductase (MADPH), mRNA
sequence.
ACCESSION B1430422
VERSION B1430422.1 GI:15207654
KEYWORDS EST.
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 925)
AUTHORS Roberts,M.C., Hendrickson,J.A., Hoffmann,D.E., Flickinger,G.H.,
Rutherford,M.S. and Mickelson,J.R.
University of Minnesota Canine Brain EST Project
Unpublished (2001)
Contact: Mickelson, J.R.

```







TITLE  
JOURNAL  
MEDLINE  
COMMENT

Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br

This sequence was derived from the PAPER/P/LICR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR2&ct=MR2-NT0135-211200-017-H09&ct3=2000-12-21&ct4=1)

Seq primer: puc 18 forward  
High quality sequence stop: 400.

FEATURES  
Source  
Location/Qualifiers

1. 400  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="NT0135"  
/dev\_stage="Adult"  
/note="Organ: nervous\_tumor; Vector: puc18; Site\_1: Sma1; Site\_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT  
ORIGIN

85 a 118 c 120 g 77 t

Query Match  
Best Local Similarity 16.0%; Score 352.4; DB 10; Length 400;  
Matches 353; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 71 gcaatgacgtgagagctcccaagaatagctgagatgtccaccccgagctgagaccctg 130  
Db 25 GCAGTGGACGTGAGAGCTCCCAAGATAGTTCGAGATGTCCACCCCGGCTGGACCCG 84

QY 131 agggagcagtgagagctccggagagatgagggcgagcttggaatctgtgacaagtgtg 190  
Db 85 AGCGGCGTGAAGAGACTCCGGGAGAGATGAGCGCGGCGATTGGAACTGTGTGACAACTGTG 144

QY 191 tctccctggaattctccctccctcgaaactgctgagggagctgtcaatctcatcgaagt 250  
Db 145 TCTCCCTGGAATTCTCCCTCCCTCGAACTGCTGAGGAGCTGTCAATCTCATCTCAAGGT 204

QY 251 ttgacggatgagcagcaggtgtgcccctctacatagacgtgacctgtgacccagcaggtg 310  
Db 205 TTGACGGATGAGCAGCAGGTGTGCCCCCTCTACATAGACGTGACCTGACACCCACGAGGTG 264

QY 311 accctgacacagaagaagaacctctctcctatgtagtcgacgaagcagccgctgaactact 370  
Db 265 ACCCTGACTAGACAAAGGAAGAACTCTCTCAATGATGATGCGCAGACCGCGCTGAACACT 324

QY 371 gtgacctggaacacatcctcacatgacatgctgtgacgctgacgacctgagagaga 424  
Db 325 GTGACCTGGAACACATCCTCACATGACCTGTGCGCTCAGCCCTCGAGAGAGA 378

RESULT 13  
LOCUS  
DEFINITION

BM089718 549 bp mRNA linear EST 19-NOV-2001  
BM089718 503548 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
COMMENT

BM089718  
BM089718.1 GI:17000346  
EST.  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

1 (bases 1 to 549)  
Smith, T.P.L., Grosse, M.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahnenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mckown, C.G., Pettea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keefe, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

2118013

Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt. trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -mismatch 12 options.

PCR primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCTCAGTCACGACG  
Plate: 5 row: D column: 9  
Seq primer: ATTGAGGTGACACTATGAG.

FEATURES  
Source  
Location/Qualifiers

1. 549  
/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="MARC 2BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="Vector: PCMV SPORT6; Site\_1: Xba1; Site\_2: Xho1; Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

BASE COUNT  
ORIGIN

112 a 166 c 149 g 122 t

Query Match  
Best Local Similarity 15.1%; Score 332; DB 10; Length 549;  
Matches 353; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 593 tggcaggttaccacaaaggccaccccgagagagcttggagctgagctgaagacact 652  
Db 161 TGGCAGGTTACCCCAAAAGCCACCTTGAAAGAGAGAGCTTTGAGGCTGATGAAAGCAC 220

QY 653 tgaaggagaagtgtatgctggagacgattcatcatcatcagcagcttctcttgaggctg 712  
Db 221 TGAAGGAGAAAGTGCTGCGAGAGCCGACCTTCATCATCACCACCTATTCTTTGGGCTG 280

QY 713 acaacatcttcgcttctgtgaaggacgtacacgacatgagcattgcccactgctc 772  
Db 281 AAACATCTCTCCGCTTGTGAAGGCTTGCTCCGAGATAGCATTAACCTGCCCATCTCC 340

QY 773 ccgggactcttcccatcagagctacacacacctctggcagctgtgtaagtgtccaaagc 832  
Db 341 CCGGCACTCTCCCAATTCAGAGGCTTACCACTCTCTCCGCACTGTGTAAATCTTCCAAAC 400

QY 833 tgaagtgtccacagagagatcaaggacgttgatgagccaatcaaaagacaagatgctgcca 892  
Db 401 TGAAGTGTCCACAGACAGATCAAGGATGTGATCGAGCCCATCAAAAGACAAAGATCTGCCA 460

QY 893 tcgcgaactatgagatgagactgtgcgctgagcctgtgtccagagagctcttgccagtgct 952  
|||||





Query Match	Similarity	14.6%	Score 320.6	DB 10	Length 550
Best Local	Similarity	85.6%	Pred No. 6.2e-60		
Matches	369	Conservative	0	Mismatches	59
				Indels	3
				Gaps	1
OY	10	gccatggtgaaagccagagaaacagcaagcctcaaccctgtcttgagggcagtgcc	69		
Db	123	gccatggtgaaagaaacccagaggaacggcaccgcccgcccgctggagggcag--c	179		
OY	70	accagtgagtgaggaagcgtcccaagatagttgagatgtccaccocggcgcttgacct	129		
Db	180	accacggcagggagagcgtcccaaggacaattcaaggctccacagccggggttgacccc	239		
OY	130	gagcgagcatgagaagactccggagagaagatgagcgcgcgatlttgaaatctgtgtacaatg	189		
Db	240	gagcgatgagagagactccggagagaagatgagcgcgcgatlttgaaatctgtgtacaatg	299		
OY	190	ttctctccggaaattttccctctctcgaaatgtctgagggagcggtcaatctcaatc	249		
Db	300	ttctctccctgaagattttccctctctcgaaatgtctgagggagcggtcaatctcaatc	359		
OY	250	tttgacccgagatgacgacgagtgagcccccctctacatagaagctgtaacctgaccccaagat	309		
Db	360	tttgacccgagatgacgacgagtgagcccccctctcttggtagagctgtaacctgaccccaagat	419		
OY	310	gacctgtgctcagaagaagagactccctccatgatgatgtgcccagacacgocgltgaactac	369		
Db	420	gattctgtgctccgaaagagacgctgctccatgagtgatggccagacacgocgltgaactac	479		
OY	370	tgtagccgagagacacatcctgacacatgacctgctgcgctcagcgctggaggaatacag	429		
Db	480	tgccgctcgcagacacatcctgcacatgacacctctgcacatcacaagccgtgaacagatcacg	539		
OY	430	ggccatctgcga	440		
Db	540	ggccacgtgaa	550		

Search completed: June 26, 2002, 16:20:11  
Job time: 6638 sec